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July 2, 2003, 07:25:01; Search time 43.3333 Seconds (without alignments) 30.750 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                     908470
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                             908470 seqs, 133250620 residues
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                US-09-673-785D-8
54
1 CVIGXSGDRC 10
                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                    Scoring table:
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/ SIDS2/goddata/geneseq/geneseqp_emb1/AA1989.DAT:*
/ SIDS2/goddata/geneseq/geneseqp_emb1/AA1990.DAT:*
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
		æ				
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
-	24	100 0	10		AAV52143	TOTAL CONCENTRATION
1	*		7	7	C#17C IUU	MOUSE EGF CELLVED
7	54	100.0	47	23	AAG66047	Mouse EGF motif se
٣	54	100.0	, 53	2	AAP40315	Epidermal growth f
4	. 54	100.0	53	10	AAP91658	Amino acid sequenc
S	54	100.0	53	11	AAR08007	Modified murine ep
9	54	100.0	53	16	AAR67275	Synthetic human/mo
7	54	100.0	53	18	AAW34466	Chimeric epidermal
80	54	100.0	53	18	AAW34467	Chimeric epidermal
6	54	100.0	53	19	AAW50134	Mouse epidermal gr
10	54	100.0	53	19	AAW50139	Epidermal growth f

Nelson J, Walker B, McFerran N, Harriott P;

Epidermal growth f Human EGF. Home s Epidermal growth f Mouse epidermal growth f Recombinant human Angiotensin conver Ret epidermal grow Human Neuregulin-2 Human transmembran Human transmembran Rat cerebellum der Human powel polytope	Human novel polype Human novel polype EGF fragment. Syn Substituted EGF fr Target peptide fro
3 19 AAW50140 3 22 AAB37612 4 23 AAB17612 4 23 AAU76704 4 23 AAU76704 6 22 AAU02933 6 22 AAU02934 6 22 AAU02934 6 22 AAU02934 6 22 AAU02936 6 22 AAU02936 6 22 AAU02936 6 22 AAU02953 7 22 AAU02953 8 22 AAB57106 8 15 AAR57106 8 15 AAR57106 8 15 AAR57106 8 23 AAB55195 6 22 AAB35195	77 77 77 77 77 77 77 77 77 77 77 77 77
54 100.0 53 54 100.0 53 54 100.0 54 54 100.0 54 54 100.0 54 54 100.0 54 54 100.0 15 55 100.0 1376 56 100.0 1376 57 100.0 1073 58 100.0 1073 59 100.0 576 50 100.0 576 50 100.0 576 51 100.0 576 52 100.0 576 53 100.0 576 54 100.0 1073 54 100.0 1073 54 100.0 1073 55 100.0 1073 56 100.0 1073 57 100.0 10	44 81.5 43 79.6 43 79.6 17.6 43 79.6 17.6 43 79.6 43 79.6 43 79.6 43 79.6 43 79.6 43 79.6 43 79.6 43 79.6
11111111111111111111111111111111111111	~ 8 9 0 1 0 1 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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Epidermal growth factor; EGF; laminin receptor; angiogenesis; medicament; wound healing; retinopathy of immaturity; metastatic cancer; candida infection; leishmania; trichomonas vaginalis.
                                                                                                                                                                                                                                                                                                                                                                                                              Mouse EGF derived peptide for targetting laminin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Acetyl-Cys (S-ACM)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Cys (S-Acm)-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                   AAY52143 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-1998; . 98GB-0008407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYBE-) UNIV QUEENS BELFAST
                                                                                                                                                                                                                                                                                                           28-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
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                                                                                                                                                                                                            AAY52143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
RESULT 1
                                                         AAY52143
                                                                                                                                                                                                            ACCOS NATIONAL STATEMENT OF A STATEM
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cc useful for regulating an endogenous protein affecting ErbB-4 receptor cc activity in vivo. They are also useful for treating or preventing a disease condition or syndrome associated with disregulation of an endogenous protein affecting ErbB-4 receptor activity, e.g., amyotrophic cc lateral solerosis (Lou Gehrig's disease), Bell's palsy, spinal muscular disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's crome, nerve deafness, neuropathy, muscular dystrophy, extramamary cc syndrome, nerve deafness, neuropathy, muscular dystrophy, extramamary cancer, cervical carcinoma, endometrial adenocarcinoma, pencreatic of another contraction and Zollinger-Ellison syndrome. The agent comprised in the pharmaceutical composition includes a polypeptide (e.g., a soluble colling of an individed colling of an immunoreactive derivative of an enceptor activity. Traceable synthetic/recombinant RRG-4-tagged molecules compassined. Sequences AdG66044-53 represent the EGF-like motifs of various
                                                                                                                                                                                                                                                                                                                                                                         47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP40315;
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                                                                                                               This is a peptide derived from mouse epidermal growth factor (EGF) composition to target laminin receptors. EGF derived peptides inhibit blood vessel formation through their antagonism of the high affinity 67bd laminin receptor found on endothelial cells. The peptide is modified in the natural sequence to prevent protease attack. The peptide is wedd in the preparation of a medicament for binding to laminin receptors as an wounds and treating anglogenic diseases, especially retinopathy of ammaturity. Other diseases treated include metastatic cancer, trichomonas vaginalis. The peptide is used family and parasitic infestations like leishmania and training the peptide is used and the state of the peptide is an endiance of include metastatic cancer, trichomonas vaginalis. The peptide are anti-anglogenic in human models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel ErbB-4 ligand, neuregulin-4 (NRG-4). NRG-4 binds to mammalian ErbB-4 receptor and can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising NRG-4 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel ErbB-4 ligand, referred as neuregulin (NRG)-4 and polynucleotide sequences encoding NRG-4, useful for upregulating or downregulating ErbB-4 receptor activity to treat Alzheimer's disease, stroke, gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ErbB-4; neuregulin-4; NRG-4; pro-NRG-4; neuroprotective; vulnerary;
cerebroprotective; vasotropic; antiparkinsonian; anticonvulsant;
                                                   New peptide derived from murine epidermal growth factor (mEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 54; DB 21; Length 10; 90.0%; Pred. No. 0.074; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                               prevent tumour cell attachment to basement membranes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG66047 standard; peptide; 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cerebroprotective; vasotropic; ant. cytostatic; nootropic; EGF; NRG-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1c; 153pp; English.
                                                                                  Claim 4; Page 28; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YEDA ) YEDA RES & DEV CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-APR-2001; 2001WO-IL00371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2000; 2000US-0553769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse EGF motif sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CVIGYSGDRC 10
                    WPI; 2000-013229/01.
                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harari D, Yarden Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-041398/05.
                                                                                                                                                                                                                                                                                                                                                                                  10 AA;
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                                                                                                                                                                                                                                                                                                                                                                               Sequence
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AAG66047
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Synthesis of epidermal growth factor polypeptide - by condensation of protected smaller peptide sequences, de:protection then oxidn. to cyclise.
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The amino acid sequence is that of an epidermal growth factor tripentacontapeptide which is synthesised by condensation of protected smaller peptide sequences. This method produces the peptide smoothly, with high purity and yield.
                 Length 47;
                                  Indels
             Score 54; DB 23;
Pred. No. 0.29;
1; Mismatches 0;
                                                                                                                                                                      Epidermal growth factor tripentacontapeptide.
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                AAP40315 standard; protein; 53 AA.
                               1;
             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim1; Page 1; 8pp; Japanese.
                      90.08;
Query Match
Best Local Similarity 90.00;
                                                                                                                                                                                                                                                                                                                                         82JP-0137128.
                                                                                                                                                                                                                                                                                                                      82JP-0137128
                                                                                                                                                     22-JUL-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                          (NNSH ) NIPPON SHINYAKU KK.
                                                 10
                                                 1 CVIGXSGDRC
                                                           33 CVIGYSGDRC
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epithelial wounds; gastric acid secrection.
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                                                                                                                                                                                                                                                                                                                                        1111:1111
33 CVIGYSGDRC
                                                                                                                                                                                                                                                                                                                               1 CVIGXSGDRC
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                                                                                                                      (CHIR-) CHIRON CORP
                          Misc-difference 11
                                                                                                                                                                                                                                                                            53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                      Nascimento CG,
                                                                                    09-MAY-1990;
                                                                                                     12-MAY-1989;
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                                                   WO9013570-A.
                                                                    15-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                            The inventors claim synthetic peptides which correspond to sequences occurring in EGF but excluding EGF. The synthetic peptides correspond to active sequences from EGF fragments: 3-14, 12-14, 12-15, 3-10, 29-37 and 33-37 (Claims 2-7 and AAP91659-P91664 resp.). The peptides are anglogenic. Their relative shortness means that they pose fewer synthesis problems than the entire EGF molecule.
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                              Amino acid sequence for naturally occurring epidermal growth factor
                                                                                                                                                                                                                                                                                                                              stimulating angiogenesis - to amino acid sequences occuring in
                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified murine epidermal growth factor; stability; storage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 10; Length 53;
Pred. No. 0.33;
L; Mismatches 0; Indels
                Score 54; DB 5; Length 53;
Pred. No. 0.33;
1; Mismatches 0; Indels
                                                                                                                                                                                      Epidermal growth factor; anglogenesis; synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified murine epidermal growth factor.
                                                                                                           AAP91658 standard; protein; 53 AA.
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                                                                                                                                                                                                                                                                           (CSIR ) COMMONWEALTH SCIENT ORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR08007 standard; protein; 53
                100.0%;
90.0%; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                             Synthetic peptide active in has sequences corresponding epidermal growth factor.
                                                                                                                                                                                                                                         88WO-AU00300
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                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                               Fig 1; 1/1; 11pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90...
Best Conservative
                                  Conservative
                                                 1 CVIGXSGDRC 10
                                                            CVIGYSGDRC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVIGYSGDRC 42
      Query Match
Best Local Similarity
''Loca' 9; Conserve
                                                                                                                                                                                                                                                                                                             WPI; 1989-068852/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                         53 AA;
AA;
53
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                                                                                                                                             29-JUN-1990
                                                                                                                                                                                                        WO8901489-A
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                                                                   33
                                                                                                                            AAP91658;
Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                        (EGF).
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                                                                                                   AAP91658
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                                                                                            RESULT
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Cell growth factor; viscoelastic solution; fibroblastic growth factor; FGF; epidermal growth factor; EGF; buffered solution; lubrication; carboxypropyl methylcellulose; cellulose gum; dextran; dextran sulphate; chondroitin sulphate; sodium hyaluronate; osmolarity; mitogenic; wound healing; cell protection; cell coating; surgery; tissue space; hydroxypropyl methylcellulose; manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The human rEGF is used to treat oversecretion of gastric acid or epithelial wound. EGF is modified to increase its chemical stability. Its storage life is improved without diminishing its biological activity. The proteins may be prepared by traditional chemical or recombinant means.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human epidermal growth factor \cdot is substituted at position 11 for greater stability and improved storage life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 54; DB 11; Length 53; Pred. No. 0.33; 1; Mismatches 0; Indels
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37
Location/Qualifiers
                                                   Q, A,
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                                                                                                                                                                                                                                                                                                                                                                              Medina-Selby A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
90.0%; F
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                                  11..11
/label= E,
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Best Local Similarity 90.v-
.--- 9; Conservative
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This is a chimeric epidermal growth factor (EGF) protein AC. This coineric EGF protein contains sequences derived from human and mouse EGF sequences. The chimeric EGF proteins can be recombinantly produced by culturing a microorganism of the genus Bacillus transformed by an expression vector containing the encoding DNA molecules. The recombinant chimeric EGF proteins exhibit a wide variety of physiological activities similar to those of naturally occurring EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epidermal growth factor; EGF; chimeric; human; mouse; recombinant.
                                                                                                                                                         Chimeric epidermal growth factor proteins - and DNA molecules for
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 54; DB 18; Length 53;
Pred. No. 0.33;
1; Mismatches 0; Indels
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/note= region C from mouse EGF"
48.53
/note= region D from human EGF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric epidermal growth factor protein ABC.
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                                                                                                                                                                                                          Claim 5; Page 26; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
90.0%; F
                                                                                                                                                                         their recombinant production
   96JP-0123970.
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- Homo sapiens.
                                   (HGET ) HIGETA SHOYU KK.
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/note=
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Best Local Similarity
'Local 9; Conserva
                                                                    Fagami H, Tanaka A;
                                                                                                      WPI; 1997-550187/51.
N-PSDB; AAT99941.
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N-PSDB; AAT99942.
                                                                                                                                                                                                                                                                                                                                                                                53 AA;
   23-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Chimeric
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Region
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                                                                                                                                                                                                                                                 The sequences given in AAR67273-76 are cell growth factors which may be used in the viscoelastic solution of the invention. The peptides are derived from fibroblastic growth factor (FGF) and epidermal growth factor (FGF). The viscoelastic solution also comprises a buffered solution which is pref. a buffered balanced salt solution, at least 1 of hydroxy or carboxypropyl methylcellulose, a cellulose gum, dextran or dextran sulphate, chondroitin sulphate, and soldum hyaluronate. It has a pH of 6-8 and an osmolarity of 200-400 mOSmol/1. The growth factors are mitogenic in vitro for a wide range of tissues and the viscoelastic soln. may be used as a surgical soln. which is in direct contact with cells undergoing wound healing. It also provides a cell protection and cell coating during surgery. The soln. provides maintenance of tissue space, hydroxypropyl methylcellulose and chondroitin sulphate lubricate the tissue, while sodium hyaluronate
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                                                                                                                                                    Viscoelastic soln. contg. hydroxypropyl methylcellulose, sodium hyaluronate, chondroitin sulphate and growth factors - used as surgical soln. to promote wound healing, e.g. of corneal cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 16; Length 53;
Pred. No. 0.33;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                       Disclosure; Column 5; 8pp; English
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90.0%; 1
 89US-0434305
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                                                                                  Lindstrom RL, Skelnik D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 90.0
Matches 9; Conservative
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- Homo sapiens.
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48..53
/note=
                                 (LIND/) LINDSTROM R L. (SKEL/) SKELNIK D.
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                                                                                                                WPI; 1995-005865/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 AA;
13-NOV-1989;
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Chimeric
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AAW34466 RESULT

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centrifugation or membrane filtration.
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                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents mouse epidermal growth factor (EGF)

from the present invention. The present invention describes a method for

the isolation of recombinant epidermal growth factor (EGF) from whole

broth. The method comprises: (a) passing a culture containing the

crotein upwards through a column containing a fluidised bed of ion

schanger, washing the ion exchanger to remove non-adsorbed material,

allowing the ion exchanger to settle, and eluting adsorbed material,

callowing the ion exchanger to settle, and eluting adsorbed protein by

passing an eluant downwards through the column; (b) filtering the eluate

through a membrane with a molecular weight cutoff of 10000, and (c)

concentrating the filtrate on a membrane with a molecular weight cutoff

of 5000. The method is for isolating recombinant human, mouse, pig or

cat EGF, or an EGF analogue with one of four defined amino acid sequences

(given in the specification), from Bacillus brevis cultures. The EGF

proteins can be recovered in high yield and high purity without the need

to pretreat the culture broth to remove the cells, e.g. by costly
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                             chimeric ECF protein contains sequences derived from human and mouse EGF sequences. The chimeric EGF proteins can be recombinantly produced by culturing a microorganism of the genus Bacillus transformed by an expression vector containing the encoding DNA molecules. The recombinant chimeric EGF proteins exhibit a wide variety of physiological activities similar to those of naturally occurring EGF.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                               chimeric epidermal growth factor (EGF) protein ABC. This
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epidermal growth factor proteins - and DNA molecules for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF; isolation; recombinant;
                                                                                                                                                                                                                                                                                        Score 54; DB 18; Length 53;
Pred. No. 0.33;
L; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; epidermal growth factor; EGF; isolatio ton exchange chromatography; Bacillus brevis.
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                                                           English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse epidermal growth factor.
                                                                                                                                                                                                                                                                                        100.0%;
90.0%; F
                    their recombinant production
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                                                      Page 26; 40pp;
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The present sequence represents a protein which has epidermal growth factor (EGF) like activity, from the present invention. The present invention of recombinant epidermal growth factor (EGF) from whole broth. The method comprises: (a) passing a culture containing the protein upwards through a column containing a culture containing the protein upwards through a column containing a disorbed material, allowing the ion exchanger to settle, and eluting adsorbed protein by passing an eluant downwards through the column; (b) filtering the eluate through a membrane with a molecular weight cutoff of 1000, and (c) concentrating the filtrate on a membrane with a molecular weight cutoff of 5000. The method is for isolating recombinant human, mouse, pig or rat EGF, or an EGF analogue with one of four defined amino acid sequences (given in the specification), from Bacillus brevis cultures. The EGF proteins can be recovered in high yield and high purity without the need to pretreat the culture broth to remove the cells, e.g. by costly centrifugation or membrane filtration.
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                                                      Gaps
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Pred. No. 0.33;
1; Mismatches 0; Indels
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Epidermal growth factor; EGF; isolation; recombinant; ion exchange chromatography; Bacillus brevis.
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     DB 19;
                            0.33;
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                                                    1; Mismatches
Score 54;
Pred. No. 0.
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90.0%; E
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                                                    9; Conservative
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       Query Match
Best Local Similarity
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Merozoite surface protein; protazoacide; vaccine; malaria; human; EGF;

epidermal growth factor

WO200063245-A2. Homo sapiens.

26-OCT-2000.

99GB-0009072. 99US-0311817. 99CA-2271451.

20-APR-1999; 13-MAY-1999; 25-MAY-1999;

(MEDI-) MEDICAL RES COUNCIL.

20-APR-2000; 2000WO-GB01558.

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The present sequence represents a protein which has epidermal growth factor (EGF) like activity, from the present invention. The present invention describes a method for the isolation of recombinant epidermal growth factor (EGF) from whole broth. The method comprises: (a) passing coulture containing the protein upwards through a column containing a disorbed material, allowing the ion exchanger to settle, and eluting a disorbed protein by passing a telunat downwards through the column; (b) of illering the eluter through a membrane with a molecular weight cutoff of 5000. The method is for isolating recombinant contains mouses, pig or rat EGF, or an EGF analogue with one of four chiman, mouses, pig or rat EGF, or an EGF analogue with one of four defined amino acid sequences (given in the specification), from Bacillus containty without the need to pretreat the culture broth to remove the very cells, e.g. by costly centrifugation or membrane filtration.
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                                                                                                                                                                                                                                                                                                                                                                               recombinant epidermal growth factor from whole broth
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                                                                                                              Epidermal growth factor; EGF; isolation; recombinant; ion exchange chromatography; Bacillus brevis.
                                                                                                                                                                                                                                                                                                                                                                                        by fluidised-bed ion-exchange chromatography
                                                                                   Epidermal growth factor analogue 4.
AAW50140 standard; protein; 53 AA.
                                                                                                                                                                                                                                                                                                                     Miyauchi A, Nemoto A, Warren B;
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                                                           (first entry)
                                                                                                                                                                                                                                                                                          (HGET ) HIGETA SHOYU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 90.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-131057/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 AA;
                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                      17-JUL-1997;
                                                           08-JUL-1998
                                                                                                                                                                                                                                                                 01-AUG-1996;
                                                                                                                                                                                 AU9728698-A.
                                                                                                                                                                                                                                                                                                                                                                              Isolation of
                             AAW50140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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AAB37612
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In present inventions useraces to non-natural variants of a C-TERMINAL non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic one third antibody that inhibits the proteolytic cone third antibody that inhibits the proteolytic cleavage of plasmodium MSP-1_4_2, and has the same affinity for at least MSP-1_4_2, compared to natural MSP-1_1_9. The non-natural variants of and can be used to treat malaria. The present invention are useful for immunising a mammal against malaria, epidermal growth factor (EGF). This sequence was used in a sequence (see ABB37608), which was used to generate the variants of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised form; monoclonal antibody alpha 340; gene therapy;
publicanal growth factor receptor; EGF; cancer; colorectal, lung; breast;
gastilc; ovarian; immune response; cytostatic; cell growth; apoptosis;
                                                                                                                                                                                                                                                        Uthaipibull C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epidermal growth factor (EGF) used in exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to non-natural variants of a C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                  Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing malaxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 54; DB 22; Length 53; 90.0%; Pred. No. 0.33; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                        Syed S,
                                                                                                                                                                                                                                            Holder A, Birdsall B, Feeney J, Morgan W,
                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE15714 standard; Protein; 53 AA.
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                                                                                                                                                                                                                                                                        WPI; 2001-015762/02.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
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Human EGF.

27-FEB-2001

Ellis JRM,

cancer

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The invention describes a method of forming (M1) chimeric polynucleotides (I). The method comprises contacting a population of polynucleotides (I). The method comprises contacting a population of a single-stranded scaffold fragments (SF) with population of donor fragments (DF) to form a complex (II) comprising at least one SF hybridised to two DFs. (II) is treated so that single stranded regions of (II) are filled in and adjacent fragments are ligated. (M1) is useful for a directed evolution process which involves forming a library of (I) that can be screened for a characteristic of interest. Subsequent rounds of directed evolution can produce chimaric polynucleotides with an improved characteristic of interest. The methods facilitate the generation of chimeric polynucleotides and do not require hybridising conor fragments to a target or full-length template. Because the chimeragenesis process does not rely upon a contiguous, full-length template, it is unnecessary to modify a template to facilitate its removal. This is the amino acid sequence of the mouse epidermal growth factor (EGF) used to demonstrate a method of in vitro recombination
                                                                                                                                                                                                                                                                                                                   Forming chimeric polynucleotide by contacting single-stranded (ss) scaffold fragment, and donor fragment populations to form hybridised complex having ss regions which are filled-in, and ligating adjacent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; epidermal growth factor; receptor; EGF; chimeric polynucleotide; directed evolution; chimeragenesis; recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 23; Length 54;
Pred. No. 0.33;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified mouse epidermal growth factor (EGF).
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                                                                                                                                                                                                         Arensdorf JJ;
                                                                                                                                                         (ENCH-) ENCHIRA BIOTECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU76706 standard; Protein; 54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 3; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
                                                                  18-JUL-2000; 2000US-219085P.
19-OCT-2000; 2000US-0691873.
19-OCT-2000; 2000US-0692732.
18-JUL-2001; 2001WO-US22640.
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Best Local Similarity 90.0
Matches 9; Conservative
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                                          18-JUL-2000; 18-JUL-2000; 19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manifacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treatment or prophylaxis of cancer after ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation schedules. The humanised form of the antibody 340 has reduced immune response against colls expressing EGF creceptor, as the original murine antibody and has increased ability to inhibit the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                    New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; epidermal growth factor; receptor; EGF; chimeric polynucleotide; directed evolution; chimeragenesis; recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 23; Length 53;
Pred. No. 0.33;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse epidermal growth factor (EGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Fig 12; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                     21-MAY-2001; 2001WO-GB02226.
                                                             19-MAY-2000; 2000GB-0011981.
24-AUG-2000; 2000GB-0020794.
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                                                                                                                                  (SCAN-) SCANCELL LTD
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Best Local Similarity
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                                                                                                                                                                                                                         WPI; 2002-062384/08.
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the invention.

Seguence

Misc-difference

ds sp.

AAU76704;

RESULT 14 AAU76704

ŏ g WO200206469-A2

24-JAN-2002

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Gaps

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PP 24-JAN-2002.

XX XX 18-JUL-2000; 2000002-218921P.
PR 18-JUL-2000; 2000002-218921P.
PR 18-JUL-2000; 2000002-218921P.
PR 18-JUL-2000; 2000002-018932.
PR 18-JUL-2000; 2000002-018932.
PR 19-OCT-2000; 2000005-0629732.
XX XX (ENCH-) ENCHIRA BIOTECHNOLOGY CORP.
XX XX (ENCH-) ENCHIRA BIOTECHNOLOGY CORP.
XX XX (ENCH-) EALOSIS.
XX XX (ENCH-) ENCHIRA BIOTECHNOLOGY CORP.
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Oy 1 CVIGXSGDRC 10 | | | | | | | | | | | 13 CVIGYSGDRC 42

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Gaps

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Score 54; DB 23; Length 54; Pred. No. 0.33; 1; Mismatches 0; Indels

100.08; 90.08; P

Query Match 100. Best Local Similarity 90.0 Matches 9; Conservative Search completed: July 2, 2003, 07:30:54 Job time: 44.3333 secs

Sequence 1, Appli Patent No. 5332669 Patent No. 5434135 Patent No. 5218093

Sequence 13, Appl Sequence 15, Appl Sequence 15, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 13, Appli Sequence 13, Appli

Sequence 15, R Sequence 13, R

Sequence:

Title:

Run on:

Searched:

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Sequence 1.5 Application US/08597545
Fatent No. 5580738
GENERAL IMPORMATION:
APPLICANT: LABORDA, Jorge
APPLICANT: LABORDA, Jorge
TITLE OF INVENTION: Neuroendocrine Tumors
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTR: USA
ZIP: 20007-5109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTE READBLE FORM:
APPLICATION NUMBER: US/08/597,545
                                                          5218093-1

US-07-885-089B-13

US-08-456-201-15

US-08-456-201-13

US-08-456-241-15

US-08-440-13

US-08-419-878B-13

US-08-419-878B-13

US-08-419-878B-13

US-08-419-878B-13

US-08-445-265A-15

US-08-446-848-15

US-08-468-846-13

US-08-468-846-13
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CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION UNMER: 05/09/93/37
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202,
TELEFAX: (202,
TELEEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
""PE: amino acids
linear
US-08-597-545-7
RESULT 1
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Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Patent No. 5332669
Sequence 2, Appli
Patent No. 5183805
Patent No. 5183805
Patent No. 5183805
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Sequence 14, Appl
Sequence 24, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 15, Appl
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                                                                                                                                                                          (without alignments)
27.584 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                   2, 2003, 07:25:01 ; Search time 10.6667 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/pcTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                        262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                    US-09-673-785D-8
54
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Match Length DB
                                                                                                                                                                                                                                                                                        1 CVIGXSGDRC 10
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Database

Result

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Gaps

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Score 54; DB 1; Length 12; Pred. No. 0.014;

Pred. No. 0.01 1; Mismatches

100.0%; 90.0%; F

Best_Local Similarity 90.0 Matches 9; Conservative

US-08-597-545-7

Query Match

1 CVIGXSGDRC 10

12

3 CVIGYSGDRC

Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli

US-07-869-176-1 US-08-284-923-1 US-08-360-841-2 US-08-861-000-1

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APPLICANT: Mullenbach, Guy T.
APPLICANT: Blaney, Jeffrey M.
APPLICANT: Blaney, Jeffrey M.
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: EXHIBITING ENHANCED BINDING AT LOW PH
TITLE OF INVENTION: EXHIBITING ENHANCED BINDING AT LOW PH
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: Intellectual Property R-440, P.O. Box 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 1; Length 53;
Pred. No. 0.056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,032B
FILLING DATE: 20-MAR-1996
CLASSIFICATION: 514
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/746,651
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCCIUNG, Barbara G
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 231.001
TELEPHONE: 510-61-2708
TELEPHONE: 510-655-3542
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Guth, Joseph H.
REGISTRATION NUMBER: 31,261
REFERENCE/DOCKET NUMBER: 0231.004
TELECHMONICATION INFORMATION:
TELECHONE: (510) 923-3888
TELEFAX: (510) 655-3542
                                        APPLICATION NUMBER: US/08/284,923 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08619032B Patent No. 6191106
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                                                                                                                                                                                                                                                                                                                                                        LENGTH: 53 amino acids
TYPE: amino acid
                    CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-284-923-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVIGXSGDRC 10
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TYPE: amino acid
STRANDEDNESS: sir
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US-08-619-032B-2
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; Sequence 2, Application US/08284923
; Patent No. 554795
; GENERAL INFORMATION:
APPLICANT: Mullenbach, Guy T
APPLICANT: Blaney, Jeffrey M
APPLICANT: Blaney, Jeffrey M
APPLICANT: Muteins of Epidermal Growth Factor
TITLE OF INVENTION: Muteins of Epidermal Growth Factor
TITLE OF INVENTION: Exhibiting enhanced binding at low ph
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton street
CITY: Emeryville
STREET: CA
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Pred. No. 0.014;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    COUNTY: WASALINGUON, D.C.
COUNTY: WASALINGUON, D.C.
ZIP: 20007-5109
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN DATA:
APPLICATION NUMBER: US/08/457,135
FILING DATE: 01-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/989,537
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                   Sequence 7, Application US/08457135
Patent No. 5644031
GENERAL INFORMATION:
TITLE OF INVENTION: Delta-Like Gene Expressed In TITLE OF INVENTION: Neuroendocrine Tumors
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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90.0%; P
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202)0, TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 90.0
Matches 9; Conservative
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; TOPOLOGY: linear
US-08-457-135-7
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                      US-08-457-135-7
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US-08-284-923-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5183805

APPLICANT: LEE, JIN S.;BLICK, MARK
APPLICANT: LEE,
TILLE OF INVENTION: BIOACTIVE EGF PEPTIDES FOR
FORMOTION OF TISSUE REGENERATION AND CANCER THERAPY
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATE: US/07/567,407
FILING DATE: 13-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LEE, JIN S.; BLICK, MARK
TITLE OF INVENTION: BIOACTIVE EGF PEPTIDES FOR
PROMOTION OF TISSUE REGENERATION AND CANCER THERAPY
                                                                                                                                                                                                                                                                                                                                                                           ; DB 2;
. 24;
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Pred. No. 0.94;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                            Score 44;
Pred. No.
                                                      SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,864A
FILLING DATE: 8-SEP-1995
CLASCIETATAMATON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/567,407
FILING DATE: 13-AUG-1990
                                                                                                                                                      NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: HUI-017
TELECOMMUNICATION INFORMATION:
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.6%;
                                                                                                                                                                                                                                TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 754 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                            81.5%;
60.0%;
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Best Local Similarity 60.0%;
Matches 6; Conservative
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 60.00
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Best Local Similarity 60.0°
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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280 CPVGYTGDRC 289
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2 CVVGYIGERC 11
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                                              OPERATING SYSTEM:
SOFTWARE: ASCII (1
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Patent No. 5912326
GENERAL INFORMATION:
APPLICANT: Chang, Han
TITLE OF INVENTION: Related thereto
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 28 State Street
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Pred. No. 0.056;
1; Mismatches 0; Indels
                                                                                               Indels
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Pred. No. 1.8;
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APPLICANT: DEDEL, THOMAS F.
TILE OF INVENTION: PROSTATE-DERIVED MITOGEN
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
PELLING DATE: 24-MAR-1989
                                                                                                                                                                                                                                              APPLICANT: DEUEL, THOMAS F.
TITLE OF INVENTION: PROSTATE-DERIVED MITOGEN
                                                                             Pred. No. 0.05
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                             Score 54;
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/356,739
FILING DATE: 24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
90.0%; I
                                                             Query Match 100.0%;
Best Local Similarity 90.0%; I
Matches 9; Conservative 1.
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70.0%;
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Best Local Similarity 90.0.
Best Son 9; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
                                                                                                                                              33 CVIGYSGDRC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 CVIGYSGDRC 42
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boston
                                                                                                                                                                                                                                     ;Patent No. 5332669
                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 53
5332669-2
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                              US-08-619-032B-2
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5332669-2
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Sequence 14, Application US/09158710

Sequence 14, Application US/09158710

Sequence 14, Application US/09158710

GENERAL INFORMATION:

APPLICANT: Klagsbrun, Michael

APPLICANT: Abraham, Judith A.

APPLICANT: Higanshiyama, Shifeki

TITLE OF INVENTION: HEPARIN BINDING MITOGEN WITH HOMOLOGY TO EPIDERWAL

TITLE OF INVENTION: GROWTH FACTOR (EGF)

TITLE OF INVENTION: GROWTH FACTOR (EGF)

CURRENT APPLICATION NUMBER: US/09/158,710

CURRENT PLILING DATE: 1999-09-22

SARLIER FILING DATE: 1993-06-15

BARLIER FILING DATE: 1993-06-15

SOFTWARE: FRILING DATE: 1990-10-16

SOFTWARE: FRILING DATE: 1990-10-16

SOFTWARE: RESERVE OF Windows Version 3.0

LENGTH: 37
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                                                                          Score 43; DB 2; Length 37;
Pred. No. 2;
3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 44, Application US/08168091A
Petent No. 5665862
GENERAL INFORMATION:
APPLICANT: Fischbach, Gerald.
APPLICANT: Falls, Douglas R.
APPLICANT: Rosen, Kenneth M.
APPLICANT: Corfas, Gabriel.
TITLE OF INVENTION: Neurotrophic Factor.
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE AND COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION NUMBER: US/08/168,091A
FILING DATE: 15-DEC-1993
                                                                          79.68;
60.08;
                                                                 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                         1 CVIGXSGDRC 10
                                                                                                                                                                                11:1: 1:11
28 CVVGYIGERC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVIGXSGDRC 10
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28 CVVGYIGERC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-158-710-14
         ; TOPOLOGY: linear
US-08-039-364-14
                                                                                                                                                                                                                                                           RESULT 12
US-09-158-710-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-168-091A-44
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STATE: MA
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APPLICANT: Klagsbrun, Michael
APPLICANT: Abraham, Judith A.
APPLICANT: Higashiyama, Shigeki
APPLICANT: Besner, Gail F.
TITLE OF INVENTION: HEPARIN BINDING MITOGEN WITH
TITLE OF INVENTION: HOMOLOGY TO EPIDERMAL GROWTH FACTOR
TITLE OF INVENTION: HOMOLOGY TO EPIDERMAL GROWTH FACTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                            Query Match
79.6%; Score 43; DB 6; Length 25;
Best Local Similarity 60.0%; Pred. No. 1.4;
Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                       Patent No. 5256643

Patent No. 5256643

Patent No. 5256643

TITLE OF INVENTION: HUMAN CRIPTO PROTEIN

NUMBER OF SEQUENCES: 18

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/530,165

FILING DATE: 29-MAY-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
COUNTRY: U.S.A.
2 ID: 0.210-2804
COMPUTER: EADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/039,364
FILING DATE: 15 JUN 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05162/002002
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PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/598,082
FILING DATE: 16 OCT 1990
ATORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-08-039-364-14
Sequence 14, Application US/08039364
Patent No. 5811393
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-6070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
  1 CVIGXSGDRC 10
                           2 CVVGYIGERC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 CVVGYIGERC 22
                                                                                                                                                                                                                                                                                                                     LENGTH: 25
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Gaps
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US-08-899-437-12

Sequence 12, Application US/08899437

Patent No. 6121415

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

COULTY: South San Francisco

STATE: California

COUNTRY: USA
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                                                                                    79.6%; Score 43; DB 1; Length 44; 60.0%; Pred. No. 2.3; tive 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC COMPATIBLE
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 3
Pred. No. 2.4;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437 FILING DATE: 24-Jul-1997 CLASSIFTCATION: 435 ATTONEY AGENT INFORMATION: NAME: Conley, Deitdfe L. REGISTRATION NUMBER: 36,487 REFERENCE/DOCKET NUMBER: 36,487 REFERENCE/DOCKET NUMBER: 91084R1 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 1000 TELECOMMUNICAT
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Job time: 12 secs
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.6%;
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                    Query Match 79.6
Best Local Similarity 60.0
Matches 6; Conservative
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COTHER INFORMATION:
US-08-899-437-12
                                                                                                                                                                                                                                                               33 CVVGYIGERC 42
                                                                                                                                                                                                                     1 CVIGXSGDRC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
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                     US-08-278-089A-24
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Sequence 24, Application US/08278089A

Sequence 24, Application US/08278089A

Sequence 24, Application US/08278089A

Patent No. 5881114

APPLICANT: Breitman, Martin L.

APPLICANT: Rossant, Janet

APPLICANT: Vamaguchi, Terry P.

TITLE OF INVENTION:

NUMBER OF SEQUENCE: 33

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.6%; Score 43; DB 1; Length 42; 60.0%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 40 King Street West
STREET: 40 King Street West
CITY: Toronto
STATE: 0ntario
COUNTRY: Canada
ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/278,089A
FILING DATE: 20-JUL-1994
CHASSIFICATION: STREET
COMPUTER: APPLICATION NUMBER: OS/08/278,089A
FILING DATE: 20-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/953,742
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Deconti, Giulio A
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: HMI-002CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
TELEPHONE: (617) 227-7501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Kurdydyk, Linda M.
REGISTRAATON NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 364-7311
TELERAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1|:|: |:||
31 CVVGYIGERC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

July 2, 2003, 07:28:49; search time 103 Seconds

(without alignments)
11.164 Million cell updates/sec

Title:

US-09-673-785D-8

Sequence:
1 CVIGXSCDRC 10

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched:
440863 seqs, 114992915 residues

Total number of hits satisfying chosen parameters:
440863

Minimum DB seq length: 0

Maximum Abs seq length: 2000000000

Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Published_Applications_AA:*

Database

Sequence 29, Appli Sequence 5, Appli Sequence 25, Appli Sequence 36, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 5, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 114, Appli Sequence 114, Appli Sequence 114, Appli Sequence 116, Appli Sequence 116, Appli Sequence 116, Appli Sequence 1176, Appli Sequence 107, Appli	
9 US-10-211-994-29 9 US-10-211-994-5 9 US-10-211-994-7 9 US-10-211-994-7 10 US-09-280-030-64 9 US-10-150-648B-32 10 US-09-903-327A-13 10 US-09-903-327A-13 10 US-09-900-449A-7 9 US-09-900-449A-7 9 US-09-900-449A-7 9 US-09-900-449A-7 9 US-10-150-648B-31 9 US-10-150-648B-31 9 US-10-150-648B-31 9 US-10-150-648B-31 9 US-10-150-648B-31 9 US-10-150-648B-31 9 US-10-150-648B-31 9 US-09-984-130-67 9 US-09-984-130-67 9 US-09-796-753-100 9 US-09-796-753-104 10 US-09-796-753-104 10 US-09-884-130-67 9 US-09-796-753-104 10 US-09-884-130-67 9 US-10-037-182-4 10 US-09-885-583-2 10 US-09-885-583-2 10 US-09-885-583-2 10 US-10-037-182-4	
1112 1112 1112 1112 1140 403 403 603 603 105 105 105 105 105 105 105 105 105 105	
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ALIGNMENTS

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Sequence 19, Application US/10138158

Sequence 19, Application US/20030036509A1

GENERAL INFORMATION:

APPLICANT: STEM CELL PHARMACEUTICALS, INC.

APPLICANT: TWANDZIK, Daniel R.

APPLICANT: FELKER, Thomas S.

APPLICANT: FELKER, Thomas S.

APPLICANT: FELKER, Thomas S.

APPLICANT: FELKER, Thomas S.

APPLICANT: FELKER, Towns S.

APPLICANT: RENO, John M.

ITILE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS AND METHODS OF USING FILE REFERENCE: STEM1110-6

CURRENT APPLICATION NUMBER: US 09/641,587

PRIOR APPLICATION NUMBER: US 09/559,248

PRIOR FILING DATE: 1000-04-26

PRIOR FILING DATE: 1000-04-26

PRIOR FILING DATE: 1000-04-26

PRIOR FILING DATE: 1000-04-26

PRIOR PAPLICATION NUMBER: US 09/459,813

PRIOR PAPLICATION NUMBER: US 09/459,855

PRIOR PELING DATE: 1999-10-13

PRIOR PELING DATE: 1999-10-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
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US-10-138-158-19
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Best Local Similarity
Matches 9; Conserv
US-10-138-158-19
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SEQ ID NO 19
LENGTH: 53
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US-09-864-675-4

US-09-864-675-4

Sequence 4, Application US/09864675

Sequence 4, Application US/09864675

Patent No. US-00200031286A1

Sequence 4, Application US-09864675

Fatent No. US-00200031286A1

TITLE OF INVENTION: MGG-2 NUCLEIC AND DIAGNOSTIC AND THERAPEUTIC METHODS

TITLE OF INVENTION: POLYPEPTIDES, AND DIAGNOSTIC AND THERAPEUTIC METHODS

FILE REFERENCE: 04585/049002

CURRENT APPLICATION NUMBER: US-09/864,675

CURRENT FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-05-23

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Nucleotide and peptide sequence of multivalent vaccine \ensuremath{\text{US-11-994-20}}
DATABASE ACCESSION NUMBER: GenBank Accession No. US20030059802Al J00380 DATABASE ENTRY DATE: 1993-04-27 RELEVANT RESIDUES: Relevant residues FROM 919 TO 1063 US-10-150-648B-30
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APPLICANT: Rengupta, Paromita
APPLICANT: Sengupta, Paromita
APPLICANT: Paragad, Sudhanand
APPLICANT: Burman, Anand C.
APPLICANT: Mukherjee, Rama
APPLICANT: Mukherjee, Rama
APPLICANT: Mukherjee, Rama
APPLICANT: Whomso, Bocky
TITLE OF INVENTION: WULTIVALENT SYNTHETIC VACCINE FOR CANCER
TITLE OF INVENTION: WUMBER: US/10/211,994
CURRENT FILING DATE: 2002-08-02
FRIOR PELLING DATE: 2002-08-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3:1
LENGTH: 112
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                                                                                                    100.0%; Score 54; DB 9; Length 145; 90.0%; Pred. No. 0.16; 1. Mismatches 0; Indels
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70.0%; Pred. No. 5.1;
tive 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/10211994 Publication No. US20030082201A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 70.0 nes 7; Conservative
                                                                                                Query Match
Best Local Similarity 90.0
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| 92 CVIGYIGERC 101
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91 CVIGYSGDRC 100
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                      US-10-211-994-20
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
PUBLICATION INFORMATION:
AUTHORS: Gray, A., Dull, T.J. and Ullrich, A.
TITLE: Nucleotide sequence of epidermal growth factor cDNA predicts a
TITLE: 128,000-molecular weight protein precursor
JOURNAL: Nature
                                                                                                                                                                                                                                                                                                                                                                                                      ORCANISM: Mus musculus
PUBLICATION INFORMATION:
AUTHORS: Gray, A., Dull, T.J. and Ullrich, A.
AUTHORS: Gray, A., Dull, T.J. and Ullrich, A.
TITLE: Nucleotide sequence of epidermal growth factor cDNA predicts a
TITLE: 128,000-molecular weight protein precursor
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                                             Sequence 33, Application US/10150648B Publication No. US20030059802A1
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90.0%; F
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SOFTWARE: Patentin version 3.1
SEQ ID NO 33
LENGTH: 53
TYPE: PRT
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SOFTWARE: Patentin version 3.1
SEQ ID NO 30
LENGTH: 145
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Best Local Similarity 90.0
Matches 9; Conservative
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33 CVIGYSGDRC 42
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VOLUME: 303
PAGES: 722-725
DATE: 1983
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PAGES: 722-725
                               US-10-150-648B-33
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Sequence 12, Application US/10215862
Publication No. US20030036166A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Godowski, Paul J.
APPLICANT: Anark, Melanie Rose
APPLICANT: Anark,
                                                                                                                                                                          APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,665
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                    Ligands and Uses Therefor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: COLLEY, Deltdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/109,206
FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/126,663
PRIOR FILING DATE: 1998-07-30
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
                                                                                     Sequence 12, Application US/09877665
Patent No. US20020164680A1
GENERAL INFORMATION:
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IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 23
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
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                                                             JS-09-877-665-12
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                                                                                                                                                                                                                                                                                                       APPLICANT: Yankovsky, N. K.

APPLICANT: Kozlov, A. P.

APPLICANT: Kozlov, A. P.

APPLICANT: Lobashev, A. V.

APPLICANT: Lobashev, A. V.

TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences; FILE REPERENCE: 2760-103

CURRENT FILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 415

SOFTWARE: Patentin version 3.1

I.RAGAMEN: PATENTIAN NOS: 415

SEQ ID NO 171

I.RAGAMEN: PATENTIAN PATENTIAN NOS: 415

SEQ ID NO 171
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Fatent No. US20020161200A1
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Abang, Dong Xiao
TITLE OF INVENTION: ELB Receptor-Specific Neuregulin Related Ligands and
TITLE OF INVENTION: USES Therefor
FILE REFERENCE: P1084R1C2
CURRENT APPLICATION NUMBER: US/10/136,573A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 09/480,977
PRIOR APPLICATION NUMBER: US 08/899,437
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 12
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                                 Gaps
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                                 Indels
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Pred. No. 36;
2; Mismatches
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Pred. No. 3.2;
3; Mismatches
      Pred. No. 13;
3; Mismatches
                                                                                                                                                                                                                                                                                           Sequence 171, Application US/10157031 Publication No. US20030108890A1 GENERAL INFORMATION:
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60.09;
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Best Local Similarity 70.0
Section 7: Conservative
Best Local Similarity 60.(
Matches 6; Conservative
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280 CPVGYTGDRC 289
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                                                                                     1 CVIGXSGDRC 10
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32 CVVGYIGERC 41
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US-10-157-031-171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                       RESULT 6
US-10-157-031-171
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32 CVVGYIGERC 41

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Gaps
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CORRESPONDENCES: 15
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 47;
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                                                                                                                                                                                                                                                                                    APPLICANT: Gearing, David P.
Busfield, Samantha J.
TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.6%; Score 43; DB 12; 60.0%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07334/022001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,241
FILING DATE: 12-Mar-2002
CLASSIFICATION: <u >CLASSIFICATION</u>
PRIOR APPLICATION: <u >cu <u <u >cu <u >cu <u <u >cu <u <u >cu <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u >cu <u <u >cu <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u >cu <u <u <u >cu <u <u <u >cu <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u <u >cu <u <u <u <u >cu <u <u >cu <u <u <u >cu <u <u <u >cu <u <u >cu <u <u <u >cu <u <u <u >cu <u <u >cu <u <u >cu <u <u <u >cu <u <u >cu <u <u >cu <u <u <u >cu <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u <u >cu <u <u <u >cu <u <u <u >cu <u <u <u
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/699,591
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                   Sequence 17, Application US/10096241
Patent No. US20020127594A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/10201945
Publication No. US20020188110A1
GENERAL INFORMATION:
APPLICANT: Maissner, Paul S.
Fuldner, Rebecca A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 47 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 617-542-50 TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 79.6
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
                                                                                                                                                                              US-10-096-241-17
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                                                                                                                                                RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windpatin (Genentech)
CURRENT APPLICATION NUMBER: US/O9/817,647
FILING DATE: 26-Mar-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.6%; Score 43; DB 10;
60.0%; Pred. No. 3.2;
live 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                           Score 43; DB 9
Pred. No. 3.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Conley, Delidie L. REGISTRATION NUMBER: 36, 487
REFERENCE/DOCKET NUMBER: 91084R1-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/107,979
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-817-647-12
PRIOR APPLICATION NUMBER: US 08/899,437
PRIOR FILING DATE: 1997-07-24
PRIOR APPLICATION NUMBER: US 60/052,019
PRIOR FILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENČE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09817647; Patent No. US20020082229A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELEPHONE: 650/225-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1-46 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650/952-9881
                                                                                                                                                                                                                                                                                                                              79.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 12
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                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 CVVGYIGERC 41
                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-862-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-817-647-12
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                                                                                                                                                                              LENGTH:
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Wed Jul 2 :00:08:19 2003

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Sequence 35, Application US/10150648B
Publication No. US20030059802Al
GENERAL INFORMATION
APPLICANT: Bilodeau-Goesseels, Sylvie
APPLICANT: John, Sushil J.
APPLICANT: Selinger, Leonard B.
APPLICANT: Selinger, Leonard B.
TITLE OF INVENTION: Mucleic acid and protein sequences of bovine epidermal growth
TITLE OF INVENTION: factor
TITLE OF INVENTION: factor
CURRENT APPLICATION NUMBER: US/10/150,648B
CURRENT APPLICATION NUMBER: 60/292,136
PRIOR APPLICATION NUMBER: 60/292,136
PRIOR FILLING DATE: 2001-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) DATABASE ACCESSION NUMBER: GenBank Accession No. US20030059802A1 X04571;
DATABASE ENTRY DATE: 1993-04-21;
RELEVANT RESIDUES: Relevant residues FROM 970 TO 1022
US-10-150-648B-35
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS: Bell, G.I., Fong, N.M., Stempien, M.M., Wormsted, M.A., AUTHORS: Caput, D., Ku, L.L., Urdea, M.S., Rall, L.B. and Sanchez-AUTHORS: Pescador, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE: Human epidermal growth factor precursor: cDNA sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Thomas, Becky
TITLE OF INVENTION: MULTIVALENT SYNTHETIC VACCINE FOR CANCER
FILE REFERENCE: U014152-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
    Length 53
                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE: expression in vitro and gene organization. JOURNAL: Nucleic Acids Research VOLUME: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9;
3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 9
Pred. No. 3.7;
3; Mismatches
                                             3; Mismatches
    Score 43;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/211,994 CURRENT FILING DATE: .2002-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/309,975
PRIOR FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10211994 Publication No. US20030082201A1
79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
LENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sengupta, Paromita
Prasad, Sudhanand
Burman, Anand C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.68;
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Best Local Similarity bu...
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mukherjee, Rama
  Query Match 79.6
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                         1 CVIGXSGDRC 10
                                                                                                                    33 CVVGYIGERC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rao, M.R.S. APPLICANT: Senguota. F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSUE: 21
PAGES: 8427-8446
                                                                                                                                                                                                  RESULT 14
US-10-150-648B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: BELIVERY
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
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; OTHER INFORMATION: Epidermal Growth Factor (EGF, mature peptide)
US-09-903-327A-9
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                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/201,945
FILING DATE: 25-Jul-2002
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/471,377
FILING DATE: 23-Dec-1999
APPLICATION NUMBER: 08/915,096
FILING DATE: <UNFOWNS/915,096
APPLICATION NUMBER: US 08/208,008
FILING DATE: 08 MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF110D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09903327A Patent No. US20020164333A1 GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R. APPLICANT: Li, Erguang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 48 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 79.6%;
Similarity 60.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                             ZIP: 20850
COMPUTER READABLE FORM:
  CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CVIGXSGDRC 10
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28 CVVGYIGERC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: PEPTIDE LOCATION: (0)...((
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-903-327A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-201-945-13
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LENGTH: 53
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2, 2003, 07:25:01 ; Search time 12_Seconds (without alignments) 80.112 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                  283224 segs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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54
1 CVIGXSGDRC 10
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                               Title:
Perfect score:
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                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

	Description	epidermal growth f		versican precursor	versican precursor	ErbB kinase activa	hypothetical prote	epidermal growth f	chondroitin sulfat	hypothetical prote	versican - pig-tai	⊣	versican precursor	Notch homolog prot	notch homolog - se	probable tenascin	mucin - rat (fragm	probable potassium	fibropellin Ia - s	epidermal growth f		hypothetical prote	Motch B protein -	cell-fate determin	probable EGF-like	integrin beta-8 ch	integrin beta-8 ch	hypothetical prote	slit-1 protein hom	notch4 - mouse
SUMMARIES	QI	EGMSMG	A35672	T14274	T42389	PC4415	T29359	EGRT	B55885	T16271	S43922	EGHU	A60979	T30201	T31070	T09070	A39321	T48539	A40136	S17294	B69300	T34396	A49175	A49128	A44074	B41029	A41029	T26972	T42218	T09059
	DB	-	7	~	7	~	~		~	~	7	Н	1	~	~	7	7	~	~	~	N	~	~	~	~	~	~	7	7	7
	Length	1217	2139	1643	3381	57	372	1133	102	264	862	1207	2409	2352	2531	4006	447	601	1064	53	57	601	1203	2471	230	768	769	1111	1531	1964
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	Score	54	49	47	47	44	44	44	43	43	43	43	43	42	42	42	41	41	41	40	40	40	40	40	39	39	39	39	39	39
	Result No.	1	7	რ	4	2	9	7	6 0	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

C; Superfamily: epidermal growth factor precursor; EGF homology; LDL receptor YWTD-con C; Keywords: duplication; growth factor; tandem repeat; transmembrane protein E;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1217/Product: epidermal growth factor proprotein, membrane-bound form #status pr F;29-1038/Domain: extracellular #status predicted <EXT>
F;29-1038/Domain: extracellular #status predicted <EXT>
F;53-22/Domain: LDL receptor YWTD-containing repeat homology <YW01>
F;93-134/Domain: LDL receptor YWTD-containing repeat homology <YW02>

versican precursor hypothetical prote hypothetical prote hypothetical prote laminin alpha 5 ch laminin alpha 5 ch hypothetical prote probable laminin a lami	ALIGNMENTS	RESULT 1 EGNEMAL growth factor precursor - mouse epidermal growth factor precursor - mouse epidermal growth factor precursor - mouse (c.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Accession: A9472; A3304; A92118; A01387 C.Accession: A9472; A3304; A92118; A01387 C.Accession: A9472; Multinga, M.; Sanchez-Pescador, R.; Fong, N.; Selby, M.; Rutte Science 21, 236-240, 1983 A.P. Soctiume 21, 236-240, 1972 A.P. Soctiume 21, 236-240, 1972 A.P. Soctiume 21, 236-240, 1973 A.P. Soctiume 236 A.P. C.R. Hash, J.H. CODen, S. A.P. A.P. Soctiume 238 A.P. Soctium 238 A.P. So
A55535 T120721 T130721 T1318295 T151426 S13860 S1318 S1318 S1318 S1823 S	ALIG	l growth factor precursor - mouse the names: urogastrone precursor musculus (house mouse) 30-Nov-1980 #sequence_revision 11-Aug 10-Nov-1980 #sequence of mouse submaxillary me 10-Nov-1980 #sequence of mouse submaxillary me 10-Nov-1980 #sequence of epidermal grc 10-Nov-1980 #sequence of epidermal grc 10-Nov-1980 #sequence of epidermal grc 10-Nov-1980 #sequence sequence of epidermal grc 10-Nov-1980 #sequence sequence of epidermal grc 10-Nov-1980 #sequence sequence sequence sequence sequence shown by these authors of scott et al.) 10-Nov-1980 #sequence shown by these authors of scott et al.) 10-Nov-1980 #sequence shown by these authors of scott et al.) 10-Nov-1980 #sequence shown by these authors of scott et al.) 10-Nov-1980 #sequence shown by these authors of scott et al.) 10-Nov-1980 #sequence shown by these authors of scott et al.) 10-Nov-1980 #sequence shown by the primary structure of epidermal growth factor. Location of the number: A92118; MuID:7402498; Ph 10-Nov-1980 #sequence in all showly factor (EGF) stim- 19-Epidermal growth factor. Location of the number: A9214 #sequence in the pancreas, set in the BE Epidermal growth factor from this
0000000000000000		rsor e pre AA9211 AA9211 i sub i i i i i i i i facture
2397 4307 117 716 1086 3106 3106 3672 3704 4544 4544 4545 108 161 161		growth factor precursor - mouenes: urogastrone precurson. Mus musculus (house mouse) -Nov-1980 #sequence_revision n: A94272; A93304; A92118; A0 1; Urdea, M.; Soluroga, M.; Saluruture of a mouse submaxill. en number: A94272; MUID:83236 i: 1-1217 <sco> i: 1-1217 <sco 1-789,="" 1049="" 178-:="" 179-:="" 1972="" 7612-7621,="" 791-1047,="" a92118;="" a92144;="" a9218="" epidee="" he="" i:="" muid:730485="" n:="" number:="" of="" of<="" primary="" protucture="" structure="" td="" ys,="" yy,=""></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco></sco>
77777777777777777777777777777777777777		facto 18 curo 18 curo 19 curo 10 cu
		1 growth factor predate are names: urogastings: usogastings: usogastin
		RESULT 1 EGMSMG epidermal growth factor precursor - mouse N; Alternate names: urogastrone precursor C; Species: Mus musculus (house mouse) C; Date: 30 Nov-1980 #sequenc_revision 11-? C; Accession: A9472; A93304; A92118; A0138 C; Accession: A9472; A93304; A92118; A0138 Science 221, 236-240, 1983 A; Title: Structure of a mouse submaxillary A; Reference number: A94272; MUD:83233630; A; Accession: A94772 A; Molecule type: mRNA A; Residues: 1-1217 CSCO> A; Cross-references: GB:J00380; NID:9192993; R; Gray, A; Dull, T; Ullrich, A. Nature 303, 722-725, 1983 A; Title: Nuclectide sequence of epidermal gA; Residues: 1-789, Y',791-1047, 'S',1049-116 A; Molecule type: mRNA A; Residues: 1-789, Y',791-1047, 'S',1049-116 A; Molecule type: mRNA A; Residues: 1-789, Y',791-1047, 'S',1049-116 A; Note: the sequence shown by these authors unerce of Scott et al.) Biol. Chem. 247, 7612-7621, 1972 A; Title: The primary structure of epidermal A; Reference number: A92118; MUID:73048516; A; Accession: A92118 A; Molecule type: protein A; Residues: 977-1029 are not required B; Molecule type: protein A; Residues: 977-1029 A; Title: Epidermal growth factor. Location A; Reference number: A92144; MUID:7405498; A; Conment: Epidermal growth factor (EGF) st gastrointestinal cell proliferation. C; Comment: The EGF precursor is found in kt C; Comment: The active growth factor from th

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C; Accession: T42389
R; Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
B; Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
J. Biol. Chem. 273, 15758-15764, 1998
A; Title: Versican V2 is a major extracellular matrix component of the mature bovinæ b
A; Reference number: 217954; MUID:98288320; PMID:9624174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Cross-references: EMBL:AF060456; NID:g3253299; PID:g3253300; PIDN:AAC24358.1
C;Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type 1sc
C;Keywords: chondroitin sulfate proteoglycan; extracellular matrix; glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIGS
F;21-3381/Product: versican, splice form V0 #status predicted <MAT>
F;57,331,352,817,965,1017;1333,1393,1437,1463,1653,1974,2045,2074,2103,2263,2290,23;6
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R;Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Ei
R;Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Ei
A;Title: A novel brain-derived member of the epidermal growth factor family that in the A;Reference number: JC5700; MUID:98006324; PMID:9348101
A;Recession: PC4415
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                         C; Accession: 114274
R; Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
J. Biol. Chem. 273, 1578-15764, 1998
A; Title: Versican V2 is a major extracellular matrix component of the mature bovin: b A; Reference number: 217954; MUID:98288320; PMID:9624174
A; Reference number: 217954; MUID:98288320; PMID:9624174
A; Retaus: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1643 <SCH>
A; Residues: 1-1643 <SCH>
A; Residues: 1-1643 <SCH>
A; Residues: 1-1643 <SCH>
A; Cross-references: EMBL:AF060458; NID:93253303; PID:93253304; PIDN:AAC24360.1
A; Experimental source: brain
C; Reywords: 91ycoprotein
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-1643/Product: versican, splice form V2 #status predicted <MAT>
F; 57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent)
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                                            versican precursor, splice form V2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            versican precursor, splice form VO - bovine
NyAlternate names: chondrolitin sulfate proteoglycan
C:Species: Bos primigenius taurus (cattlas)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-May-2000
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C;Date: 10-Dec-1997 #sequence_revision 10-Dec-1997 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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80.0%; Pred. No. 13;
ive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: T42389
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3381 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 2
Pred. No. 6.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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F;1064-1217/Domain: intracellular #status predicted <INT>
F;347-360,366-377,373-386,388-401,407-418,414-427,429-442,445-457,453-467,469-482,751-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A35672
R;Tepass, U; Theres, C; Knust, E.
Cell 61, 787-799, 1990
A;Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as Cys, and TAT for residu
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C.Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                         <YW05> <YW06>
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A;Molecule type: mRNA
A;Residues: 1-2139 (TFP>
A;Cross-references: GB:M33753
A;Note: the authors translated the codon GGC for residue 1928
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A;Cenos. references: FlyBase: FBgn0000368
C;Superfaully: unassigned EGF-related proteins; EGF homology
C;Superfaully: unassigned EGF-related proteins; EGF homology < EGX1>
F;352-385/Domain: EGF homology < EGX1>
F;691-722/Domain: EGF homology < EGF1>
F;691-722/Domain: EGF homology < EGF5>
F;767-799/Domain: EGF homology < EGF5>
F;1878-1914/Domain: EGF homology < EGF3>
            LDL receptor YWTD-containing repeat LDL receptor YWTD-containing repeat
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                                         L receptor YWTD-containin
L receptor YWTD-containin
L receptor YWTD-containin
F homology %EG2>
F homology <EG3>
F homology <EG4>
F homology <EG4>
F homology <EG4>
F;135-176/Domain: LDL receptor YWTD-con
F;218-26/Domain: LDL receptor YWTD-con
F;263-307/Domain: LDL receptor YWTD-con
F;324-360/Domain: EGF homology #status
F;366-401/Domain: EGF homology &EG2>
F;407-44/Domain: EGF homology &EG3>
F;465-42/Domain: EGF homology &EG4>
F;486-95/Domain: EGF homology &EG4>
F;486-95/Domain: LDL receptor YWTD-con
F;530-52/Domain: LDL receptor YWTD-con
F;530-57/Domain: LDL receptor YWTD-con
F;616-659/Domain: LDL receptor YWTD-con
F;616-659/Domain: LDL receptor YWTD-con
F;610-70/Domain: LDL receptor YWTD-con
F;610-70/Domain: EGF homology &EG5>
F;812-875/Domain: EGF homology &EG6>
F;813-958/Domain: EGF homology &EG8>
F;937-1029/Product: EGF homology &EG8>
F;927-1029/Product: EGF homology &EG9>
F;927-1029/Product: EGF homology &EG9>
F;927-1029/Product: EGF homology &EG9>
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571 CAVGYSGDRC 580
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Matches 9; Conserv
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Les 7; Conserv
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Best Local S:
Matches 7
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RESULT 3

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A; Recession: S01974
A; Molecule type: mRNA
A; Residues: W, 966, *RML', 970-1023, 'NW', 1026-1108 < DOR>
A; Cross.references: EMBL: X12748
A; Molecule type: mRNA
A; Residues: W, 966, *RML', 970-1023, 'NW', 1026-1108 < DOR>
A; Cross.references: EMBL: X12748
B; Simpson, R.J.; Smith, J.A.; Moritz, R.L.; O'Hare, M.J.; Rudland, P.S.; Morrison, J Eur. J Blochem: 153, 629-637, 1985
A; Title: Rat epidermal growth factor: complete amino acid sequence.
A; Reference number: A25425; MUD: 86081810; PMID: 3000782
A; Reference number: A25425
A; Molecule type: protein
A; Residues: 974-1021 < S12>
A; Rishih, N.; Shinizu. C.; Okutani, T.; Ragawa, Y.; Takasuga, H.; Suno, M.; Wada, F. Biochim. Biophys. Acta 1095, 268-275, 1991
A; Reference number: S18419; MUID: 92069070; PMID: 1986699
A; Atcession: S18419
A; Status: preliminary
A; Molecule type: protein
A; Residues: 974-1021 < NIS>
B; Nexo, E.; Jorgensen, P.E.; Thim, L.; Roepstorff, P.
Bjochhim. Biophys. Acta 1037, 388-393, 1990
A; Title: Purification and characterization of a low and a high molecular weight form A; Reference number: S08288; MUID: 90181442; PMID: 2310752
A; Accession: S08288
A; Molecule type: Protein
A; Reference number: S08288; MUID: 90181442; PMID: 2310752
A; Accession: S08288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/Rolecule type: protein
A/Rolecules: 974-1024 <NEX>
C/COmment: Epidermal growth factor (EGF) stimulates the proliferation and differenti gastrointestinal cell proliferation.
C/COmment: EGF is released in the pancreas, small intestine, mammary gland, and (in C/Comment: EGF is released in the pancreas; small intestine, mammary gland, and (in C/Comment: EGF is released in the pancreas; small intestine, mammary gland, and (in C/Comment: EGF is released in the pancreas; EGF homology; LDL receptor YWTD-COC; Reywords: duplication; growth factor; mitogen; tandem repeat; transmembrane protein F; 12-100 formin: signal sequence #status predicted <EGT>
F; 12-1035/Domain: EDL receptor YWTD-Containing repeat homology <YW01>
F; 47-86/Domain: LDL receptor YWTD-Containing repeat homology <YW04>
F; 11-122/Domain: LDL receptor YWTD-Containing repeat homology <YW05>
F; 13-257/Domain: LDL receptor YWTD-containing repeat homology <YW05>
F; 258-302/Domain: LDL receptor YWTD-containing repeat homology <YW05>
F; 258-302/Domain: LDL receptor YWTD-containing repeat homology <YW05>
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F;1061-1133/Domain: intracellular #status predicted <INT>
F;342-355,361-372,368-381,383-396,402-413,409-422,424-437,440-452,448-462,464-477,74
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A; Reference number: S01974; MUID:89016634; PMID:3262867
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YWTD-containing repeat
YWTD-containing repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor long repeat <LR2>
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Matches 7; Conserv
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697-739/Domain:
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C;Species: Rattus norvegicus (Morway rat)
C;Date: 31-Dec-1988 *sequence_revision 14-Aug-1998 *text_change 18-Jun-1999
C;Accession: 152995; S05074; S01974; A25425; S18419; S08288
R;Saggi, S.J.; Safirstein, R.; Price, P.M.
DNA Cell Biol. 11, 481-487, 1992
A;Title: Cloning and Sequencing of the Rat Preproepidermal Growth Factor CDNA: Comparisc
A;Reference number: 152995; MUID:92398779; PMID:1524680
                                                  A. Experimental source: PC-12 cell
C. Comment: This protein is a member of the epidermal growth factor family. It is functic ating the differentiation of MDA-MB-453 cells.
C. Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology
F.1-25/Domain: EGF homology (fragment) < EGF>
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A;Residues: 'W', 966, 'RWL', 970-1023, 'NW', 1026-1108, 'SGAGVSSGPQPWFVVLE', 1126, 'HQ' <
A;Cross-references: EMBL:X12748
R;Dorow, D.S.; Simpson, R.J.
Nucleic Acids Res. 16, 9338, 1988
A;Title: Cloning and sequence analysis of a cDNA for rat epidermal growth factor.
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A;Molecule type: DNA
A;Residues: 1-372 <MUR>
A;Residues: 1-372 <MUR>
A;Cross-references: EMBL:US8746; PIDN:AAB00626.1; GSPDB:GN00022; CESP:R05G6.9
A;Experimental source: strain Bristol N2; clone R05G6
                          A;Cross-references: DDBJ:D89997; NID:g2605633; PIDN:BAA23346.1; PID:g2605634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29359
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A;Residues: 1-1133 <RES>
A;Cross-references: EMBL:U04842; NID:g440236; PIDN:AAB60436.1; PID:g440237
R;Simpson, R.
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submitted to the EMBL Data Library, May 1996
A:Pescription: The sequence of C. elegans cosmid R05G6.
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                                                                                                                                                                                                                                                Score 44; DB 2;
Pred. No. 1;
3; Mismatches
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60.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 80/1; 161/1; 245/1; 286/1
                                                                                                                                                                                                                                                   81.5%;
60.0%;
                                                                                                                                                                                                                                                Query Match 81.5
Best Local Similarity 60.0
Matches 6; Conservative
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Matches 6; Conservative
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233 CYLGYSGDKC 242
                                                                                                                                                                                                                                                                                                                                                                           1 CVIGXSGDRC 10
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CPVGYTGDRC 25
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A;Gene: CESP:R05G6.9
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Gaps

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A; Note: the authors translated the codon occ los lesions of as Asn
659 as Asn
67. Superfamily: versican; C-type lectin homology; complement factor H repeat homology, C; Superfamily: versican; C-type lectin homology; complement factor H repeat homology; C; Reywords: chondroitin sulfate proteoglygan; extracellular matrix
F: 137/Domain: link protein repeat homology (fragment) <LNK1>
F: 781-137/Domain: Lore homology cEG1>
F: 722-753/Domain: EGF homology <EG2>
F: 760-791/Domain: EGF homology <EG2>
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A;Residues: 829-834, X',836-839, X',841-845, X',847-848 <TSU>
A;Residues: 829-834, X',836-839, X',841-845, X',847-848 <TSU>
A;Rote: this is the amino-terminal sequence of a high molecular weight form of EGF_1
B;Sybooda, M.; Bauhofer, A.; Schwind, P.; Bade, E.; Rasched, I.; Przybylski, M.
Biochim. Biophys. Acta 1206, 35-41, 1994
A;Title: Structural characterization and biological activity of recombinant human epi
A;Reference number: S45282; MUID:94242778; PMID:8186248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Wolecule type: protein
A; Residues: 'MKKYP', 970-1023 <SV2>
A; Residues: 'MKKP', 970-1023 <SV2>
A) Note: expressed recombinant protein
C; Comment: Epidermal growth factor (EGF) stimulates the proliferation and differentia gastrointestinal cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N'Alternate names: urogastrone precursor.
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Nov-1980 #sequence_revision 14-Aug-1998 #text_change 08-Dec-2000
C;Date: 30-Nov-1980 #sequence_revision 14-Aug-1998 #text_change 08-Dec-2000
C;Accession: A25531; A01388; A35517; A29721; S45283
R;Bell, G.I.; Fong, N.M.; Stemplen, M.M.; Wormsted, M.A.; Caput, D.; Ku, L.; Urdea. Mucleic Acids Res. 14, 8427-8446, 1986
A;Title: Human epidermal growth factor precursor: cDNA sequence, expression in vit.:o
A;Reference number: A25531; MUID:87066721; PMID:3491360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 971-1023 <FUR>
R;Tsukumo, K.; Nakamura, H.; Sakamoto, S.
Biocham. Biophys. Res. Commun. 145, 126-133, 1987
A;Title: Purification and characterization of high molecular weight human epiderma 9
A;Reference number: A29721; MUID:87241488; PMID:3297054
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A; Residues: 971-1023 <GRE>
A; Note: some of the molecules lack Arg-1023
A; Note: some of the molecules lack Arg-1023
B; Puruya, M.; Akashi, S.; Hirayama, K.
Biochem. Biophys. Res. Commun. 163, 1100-1106, 1989
A; Title: The primary structure of human EGF produced by genetic engineering, studiæd A; Reference number: A33517; MUID:89391964; PMID:2789514
A; Accession: A33517
A,Note: 507-Ser was also found A,Note: the authors translated the codon GCC for residue 50 as Val, AAG for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1207 < UNIT CONSTRUCTORS TEACHERS
A; Cross-references: EMBLS.X4571; NID:g31120; PIDN:CAA28240.1; PID:g31121
A; Note: 708-Met was also found
A; Note: intron positions were also determined
A; Forey, H; Preston, B.M.
A; Title: The primary structure of human urogastrone.
A; Reference number: A01388; MUID:77117897; PMID:300079
                                                                                                                                                                                                                                                                                                                                                                              Length 862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 18;
2; Mismatches
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A; Note: expressed recombinant protein
A; Accession: S45283
                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.6%;
Best Local Similarity 70.0%;
Matches 7; Conservative
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                                                                                                                             C; Species: Homo sapiens (man)
C; Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 16-Jul-1999
C; Accession: B55885
R; Zako, M.; Shlomura, T.; Ujita, M.; Ito, K.; Kimata, K.
J. Biol. Chem. 270, 3914-3918, 1995
A; Title: Expression of PG-M(V3), an alternatively spliced form of PG-M without a chondre A; Reference number: A55885; MUID:95181355; PMID:7876137
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Submitted to the EMBL Data Library, June 1995

Submitted to the EMBL Data Library, June 1995

A; Description: The sequence of C. elegans cosmid F35D2.

A; Reference number: 218488

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Accession: T1627

A; Molecule type: DNA

A; Residues: 1.264 <CON>

A; Residues: EMBL:U28741; NID:g861290; PID:g861291; PIDN:AAA68325.1; CESP:F35D2.:

A; Experimental source: strain Bristol N2

C; Genetics:
A; Experimental source: strain Bristol N2

A; Gene: CESP:F35D2.3

A; Introns: 40/3; 71/3; 160/3; 197/3
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A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-102 cZAX>
A.Cross-references: GB:S75879; GB:D32039
C.Superfamily: versican; C-type lectin homology; complement factor H repeat homology;
F; 24-55/Domain: EGF homology <EG2>
F; 62-93/Domain: EGF homology <EG2>
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N.Alternate names: chondroitin sulfate proteoglycan

S.Species: Macaca nemestrina (pig-tailed macaque)

C.Species: Macaca nemestrina (pig-tailed macaque)

C.Species: Macaca nemestrina (pig-tailed macaque)

C.Accession: S4392

S.Raco, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.

Matrix Biol. 14, 213-225, 1994

A.Title: Identification of the proteoglycan versican in aorta and smooth muscle cells h. A. Reference number: S43921; MUID:95005762; PMID:7921538

A.Rocession: S4392

A.Rocession: S4392
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16271
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                                                                                               chondroitin sulfate proteoglycan MV3 - human (fragment)
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1; Mismatches
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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46 CVPGYSGDQC 55
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76 CPYGLSGDRC 85
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A;Residues: 208-440;1094-1385;1910-2246 <YAO>
R;Bygnami, A.; Lane, W.S.; Andrews, D.; Dahl, D.
R;Bygnami, A.; Lane, W.S.; Andrews, D.; Dahl, D.
A;Bygnami, A.; Lane, W.S.; Andrews, D.; Dahl, D.
A;Title: Structural similarity of hyaluronate binding proteins in brain and cartilag A;Reference number: A60979; MUID:89229983; PMID:2469524
                                                                                                                                                                                                                                                                         A; Accession: A60979
A; Molecule type: protein
A; Accession: A60979
A; Molecule type: protein
A; Residues: 171-210/289-303 <BIG>
A; Molecule type: protein
A; Residues: 171-210/289-303 <BIG>
A; Molecule type: protein
B; Perides, G; Lane, W.S.; Andrews, D.; Dahl, D.; Bignami, A.
B; Perides, G; Lane, W.S.; Andrews, D.; Dahl, D.; Bignami, A.
J; Biol. Chem. 264, 5981-5987, 1989
A; Reference number: A30388; MUID:89174663; PMID:2466833
A; Accession: A30388; MUID:89174663; PMID:2466833
A; Residues: 24-50;80-87, D', 89-119;128-155;167-218;229-259, IR';261-268;277-283, 'G', R; Krusius, T.; Gehlsen, K.R.; Ruoslahti, E.
J; Biol. Chem. 262, 13120-13125, 1987
A; Title: A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-A; Reference number: A29348; MUID:88007514; PMID:2820964
A; Residues: 1725, 'V', 1727-2409 <KRU>A; Residues: 1725, 'V', 1727-2409 <KRU>A; Residues: 1725, 'V', 1727-2409 <KRU>A; Residues: 1725, 'V', 23883-23887, 1992
A; Reference number: A45131; MUID:93054750; PMID:1429726
A; Reference number: A45131; MUID:93054750; PMID:1429726
A; Residues: 21-22, 'X', 24-37 <PEZ>
A; Residues: 21
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R;lozzo, R.V.; Naso, M.F.; Cannizzaro, L.A.; Wasmuth, J.J.; McPherson, J.D.
Genomics 14, 4845-851, 1992
A;Title: Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human A;Reference number: 154179; MUID:93122792; PMID:1478664
A;Accession: 154179
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 251-347 <RES>
A;Cross-references: GB:S52488; NID:9263313; PIDN:AAB24878.1; PID:9263314
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A, Cross-references: GDB:L27873; OMIM:118661
A, Cross-references: GDB:L27873; OMIM:118661
A, Map position: 5q12-5q14
C, Superfamily: version: C-type lectin homology; complement factor H repeat homology
F;1-20/Domain: signal sequence #status predicted <SIG>F;1-240/Protodct: proteoglygan 24K core protein #status predicted <MAT>F;265-346/Domain: link protein repeat homology <LINK1>F;265-346/Domain: link protein repeat homology <LINK2>F;559-4654/Domain: EGF homology <EG2>F;2106-2137/Domain: EGF homology <EG2>F;2106-2137/Domain: EGF homology <EG2>F;2106-2137/Domain: C-type lectin homology <LINK2>F;2162-2302/Domain: C-type lectin homology <EGH>F;2182-2302/Domain: C-type lectin homology <EGH
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C;Species: Halocynthia roretzi
C;Species: Halocynthia roretzi
C;Species: T3000 #sequence_revision .02-Sep-2000 #text_change .02-Sep-2000
C;Accession: T30201
R;Hori, S.; Saltoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.
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      Residues: 208-440;1094-1385;1910-2246 <YAO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No
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70.0%;
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Matches 7; Conservative
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T30201
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                                                                                                                                                                                                                                                 A;Cross reterences: with the control of the control
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1058-1207/Domain: intracellular #status predicted <INT>
318-330,325-339,341-354,360-371,367-380,382-395,401-412,408-421,423-436,439-451,447-46
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C;Comment: EGF is released in the pancreas, small intestine, mammary gland, and (in some C;Comment: The EGF precursor is found in kidney as a receptor-like membrane-bound protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan N.Contains: glial hyaluronate-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-2409 < ZINA
A; Residues: 1-2409 < ZINA
A; Cross references: GB: XI5998; NID: 937662; PIDN: CAA34128.1; PID: 937663
A; Cross references: GB: XI5998; NID: 937662; PIDN: CAA34128.1; PID: 937663
B; Yao, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
A; Xiao, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
A; Xiao, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
A; Title: Identification of the proteoglycan versican in aorta and smooth muscle cells
A; Reference number: S43921; MUID: 95005762; PMID: 7921538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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C;Species: Homo saplens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: S06014; S43921; A60979; A30358; A29348; A45131; I54179
EMBO J. 8, 2975-2981, 1989
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A;Accession: S06014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                     A; Cross-references: GDB:119105; OMIM:131530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              976-1012/Domain: EGF homology <EG9>
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A; Molecule type: mRNA
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Dev. Genes Evol. 207, 371-380, 1997

A.Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the cer A.Reference number: 220775

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Status: 1-2352

A.Gross-references: EMBL:AB001327; NID:d1204472; PID:d1026501; PIDN:BAA25571.1

A.Gene: Notch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Sherwood, D.R.; McClay, D.R.;
Development 124, 3363-3374, 1997
A;Title: Identification and localization of a sea urchin Notch homologue: insights into A;Reference number: Z20966; MUID:97454256; PMID:9310331
A;Status: preliminary; translated from CB/ZMAD; Annon Application 23.070
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R) Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc Submitted to the EMBL Data Library, October 1997
A) Description: Sequence of the mouse major histocompatibility locus class III region.
A) Reference number: 216543
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A;Map position: 17
A;Map position: 17
A;Introns: 124/1; 735/1; 773/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 1440/1; 15
019/1; 3115/1; 3208/1; 3302/1; 3405/1; 3517/1; 3558/1; 3606/1; 3646/1; 3694/1; 3737/3; 3
C;Superfamily: tenascin.X; EGF homology; fibrinogen beta/gamma homology; fibronectin type F;422-448/Domain: EGF homology EEGF>
F;826-906/Domain: EGF homology EEGF>
F;826-906/Domain: fibronectin type III repeat homology <3FR>
F;3789-3997/Domain: fibrinogen beta/gamma homology <FEGS>
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A; Molecule type: mRNA
A; Residues: 1-2531 <SHE>
A; Residues: 1-2531 <SHE>
A; Cross-references: EMBL:AF000634; NID:g2570350; FID:g2570351; PIDN:AABB2088.1
C; Superfamily: notch protein; ankyrin repeat homology; EGF homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Lytechinus variegatus (variegatus)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C;Accession: T31070
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C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
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Pred. No. 65;
1; Mismatches 2; Indels
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77.8%; Score 42; DB 2; Length 2531;
Best Local Similarity 60.0%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 2; Indels
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A/Molecule type: DNA
A).Residues: 1-4006 <ROW>
A).Residues: 1-4006 <ROW>
C).Genetics: EMBL.AF030001; NID:92564945; PID:92564958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sea urchin (Lytechinus variegatus)
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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615 CPVGTSGDNC 624
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2, 2003, 07:26:26 Search completed: July Job time: 14 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 2, 2003, 07:25:02; Search time 10.3333 Seconds (without alignments) 40.138 Million cell updates/sec Run on:

US-09-673-785D-8 54 1 CVIGXSGDRC 10 Title: Perfect score: Sequence: BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	P01132 mus musculu	P10040 drosophila	P81282 bos taurus	P56974 mus musculu	P07522 rattus norv	Q28858 macaca neme	homo	рошо	Q90y57 brachydanio	P10079 strongyloce	Q9r0m0 mus musculu	Q00968 sus scrofa	O29845 archaeoglob	_	Q04721 homo sapien		P37789 shigella fl	Q01083 drosophila	P26013 oryctolagus		P31695 mus musculu	Q9erb4 rattus norv	_		_	-	Q00174 drosophila	Q61001 mus musculu	Q07954 homo sapien	Q04571 neurospora	P18844 xenopus lae	4	Q8x9z2 escherichia
SUMMARIES	ΙD	EGF_MOUSE	CRB_DROME	PGCV_BOVIN	NRG2_MOUSE	EGF_RAT	PGCV_MACNE	EGF_HUMAN	PGCV_HUMAN	JAG1_BRARE	FBP1_STRPU	CLR2_MOUSE	EGF_PIG	Y402_ARCFU	NTC2_MOUSE	NTC2_HUMAN	NTC2_RAT	YRF3_SHIFL	SPIT_DROME	ITB8_RABIT	ITB8_HUMAN	NTC4_MOUSE	PGCV_RAT	PGCV_MOUSE	YEP2_SCHPO	LMA2_MOUSE	LML2_CAEEL	L.M.A_DROME	LMA5_MOUSE	LRP1_HUMAN	RODL_NEUCR	7B2_XENLA	MURE_YERPE	MURE_ECO57
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æ	Query Match	100.0			81.5				79.6		•	75.9							72.2		٠.	72.2		72.2	•		٠.	٠.	٠.		ω.	ω.		68.5
	Score	54	49	47	44	44	43	43	43	42	41	41	40	40	40	40	40	39	39	39	39	39	39	39	38	38	38	38	38	38	37	37	37	37
	Result No.	1	7	m	4	2	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P22188 escherichia P57815 pasteurella	Q8z9h3 salmonella Q8zru7 salmonella	Q8ywfO anabaena sp P54792 homo sapien	Q08761 mus musculu P35739 rattus norv	Q90y54 brachydanio Q99466 homo sapien	Q9r172 rattus norv P46530 brachydanio	•
MURE_ECOLI	MURE_SALTI MURE_SALTY	MURE_ANASP DVLL_HUMAN	PRTS_MOUSE TRKA_RAT	JAG3_BRARE	NTC3_RAT	
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ALIGNMENTS

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NOT REQUIRED FOR FULL BIOLOGICAL ACTIVITY
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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STRAIN-Oregon-R; TISSUE-Embryo;
MEDLINE-90263104; PubMed-2344615;
Tepass U., Theres C., Knust E.;
Tcrumbs encodes an EGF-11ke protein expressed on apical membranes of Drosophila epithelial cells and required for organization of epithelia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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MEDLINE-87218537; PubMed-3107986;
Knust E., Dietrich U., Tepass U., Bremer K.A., Weigel D.,
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01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                   WEDLINE-99180407; PubMed-10082370;
MEDLINE-99180407; PubMed-10082370;
MEDLINE-99180407; PubMed-10082370;
MEDLINE-99180407; PubMed-10082370;
MEDLINE-99180407; PubMed-10082370;
MICE E.C., Norton R.S.; A.A., Alewood D., Alewood P.F., Domagala T.,
MICE E.C., Norton R.S.; A.M., Alewood D., Alewood P.F., Domagala T.,
MICE E.C., Norton R.S.; A.M., Alewood D., Alewood P.F., Domagala T.,
MICE E.C., Norton R.S.; Alewood D., Alewood P.F., Domagala T.,
MICE E.C., Norton R.S.; Alewood D., Alewood P.F., Domagala T.,
MICH R. A., Alewood D., Alewood D., Alewood P.F., Domagala T.,
MICH E.C., Morton R.S.; Alewood D., Alewood P.F., Domagala T.,
MICH E.C., Morton R.S.; Alewood D., Alewood 
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DR PIR; A01387; EGRESAG.

DR PIR; A01387; EGRESAG.

DR PDB; 1EGF; 31-JAN-94.

DR PDB; 1EGF; 31-JAN-94.

DR PDB; 1EFP; 31-JAN-94.

DR PDB; 1EPP; 31-JAN-94.

DR PROSIDE; PRO00135; EGF_1.

DR PRINTS; PRO0009; EGF_TGF.

DR PRANT; SM000135; LY; 9.

DR SWART; SM00135; LY; 9.

DR PROSITE; PS00110; EGF_11ke; 7.

DR PROSITE; PS001187; EGF_2.

DR PROSITE; PS001187; EGF_2.

DR PROSITE; PS001187; EGF_2.

DR PROSITE; PS01187; EGF_2.

DR PROSITE
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EGF-LIKE 1 (INCOMPLETE).
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EXTRACELLULAR (POTENTIAL).
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EMBL; V00741; CAA24115.1; ALT_FRAME.
EMBL; V00741; CAA24116.1; -.
   Biochemistry 31:11928-11939(1992)
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CYTOPIASMIC (POTENTIAL).
EGF-LIKE 1.
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CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 14.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 14.
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              domain; Transmembrane,
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EMBL; X05144; CAA28793.1; ...
PIR; BA6637; B26637.
PIR; A35672.
HSSP; P00740; 1EDM.
FlyBase; FBGN0000368; crb.
InterPro; IPR001051; ASx_bydroxyl.
InterPro; IPR001051; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00138; EGF_II.
InterPro; IPR00198; EGF_II.
InterPro; IPR00198; EGF_II.
Pfam; PF00069; EGF; 26.
Pfam; PF00069; EGF; 26.
Pfam; PF00010; EGF100D.
SWART; SW00001; EGF2; 11.
SWART; SW00001; EGF_CA; 12.
PROSITE; PS000186; EGF_2; 17.
PROSITE; PS00186; EGF_2; 17.
PROSITE; PS00186; EGF_2; 17.
PROSITE; PS00187; EGF_OMAIN; 3.
DIfferentiation; Repeat; EGF_11ke domain; Glycoprotein; Signal; Phosphorylation.
  Vaessin H., Campos-Ortega J.A.;
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                                                connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
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LINK 2.
LOGA ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
DOMAIN).
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SIGNAL 21 3381 VERSICAN CORE PROTEIN.
DOMAIN 37 138 IG-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR000152; Asx_hydroxyl.
InterPro: IPR000561; EGF-like.
InterPro: IPR000761; EGF_2.
InterPro: IPR001881; EGF_Ca.
InterPro: IPR003599; IG.
InterPro: IPR003066; Ig_MRC.
InterPro: IPR003066; Ig_MRC.
InterPro: IPR003066; Ig_MRC.
InterPro: IPR000380; Link.
InterPro: IPR000388; Link.
InterPro: IPR000436; Sushi_SCR_CCP.
Fam: PF00008; EGF; 2.
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SMART; SMO0032; CCP; 1.
SMART; SMO01034; CLECT; 1.
SMART; SMO0109; EGF_2.
SMART; SMO0409; EGF_2.
SMART; SMO0409; EGF_1.
SMART; SMO0409; EGF_1.
SMART; SMO0445; LINK; 2.
PROSITE; PSO0010; ASX_HYDROXXL; 1.
PROSITE; PSO0045; C_TYPE_LECTIN_1; 1.
PROSITE; PSO0045; C_TYPE_LECTIN_2; 1.
PROSITE; PSO1186; EGF_1; 2.
PROSITE; PSO1186; EGF_1; 2.
PROSITE; PSO1186; EGF_2; 1.
PROSITE; PSO1186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF060456; AAC24358.1; -. EMBL; AF060457; AAC24359.1; -. EMBL; AF060459; AAC24360.1; -. EMBL; AF060459; AAC24361.1; -. HSSP; P01132; 1EPG.
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Pfam; PF00193; Xlink; 2.
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TISSUE-Spinal cord;
MEDIINE-92062692; PubMed-1720020;
Perides G., Biviano F., Bignami A.;
"Interaction of a brain extracellular matrix protein with hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mature
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGCV_BOVIN STANDARD, PRT, 3381 AA.
P81282, 0776019, 0776119, 077612,
15-DEC-1998 (Rel. 37, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
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Schmalfeldt M., Dours-21mmermann M.T., Winterhalter K.H.,
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BY SIMILARITY.
BY SIM
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Pred. No. 0.72;
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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571 CAVGYSGDRC 580
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M MGD; MAI:1098246; NR92.

R InterPro; IPR000561; EGF-like.

R InterPro; IPR000561; EGF-like.

R InterPro; IPR0003598; Ig_c2.

R InterPro; IPR00154; Neuregulin.

R Pfam; PP00004; EGF; 1.

R Pfam; PP000184; EGF; 1.

R SMART; SM00184; EGF; 1.

R SMART; SM00184; EGF; 1.

R PROSITE; PS01186; EGF_1; 1.

R PROSITE; PS01186; EGF_2; 1.

R Transmembrane; Multigene family; Alternative splicing.

R PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTECLYTIC PROCESSING. REGULATION OF THE PROTECLYTIC PROCESSING OF THE PROTECLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN DIMERLALION (BY SIMILARITY).

DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chearacterization of a neuregulin related gene, Don-1, that is highly expressed in restricted regions of the cerebellum and hippocampus."; Mol. Cell. Biol. 17:4007-4014(1997).

**Noticell. Biol. 17:4007-4014(1997).

**INCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS, RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND ACTIVATION OF THE ERBB RECEPTORS. MAY ALSO PROMOTE THE HETERODIMERIZATION WITH THE EGF RECEPTOR.

**INCOMPLY OF THE FOR PROSECTION. AND AS A PROTECLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS A PROTECLYICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).

**INCOMPLY OF THE FORM TO SEEM TO BE ACTIVE (BY SIMILARITY).

**INCOMPLY OF THE FORM TO SEEM TO BE ACTIVE (BY SIMILARITY).

**INCOMPLY OF THE FORM TO SEEM TO BE ACTIVE (BY SIMILARITY).

**INCOMPLY OF THE FORM TO SEEM TO BE ACTIVE (BY SIMILARITY).

**INCOMPLY OF THE FORM TO SEEM TO BE ACTIVE (BY SIMILARITY).

**INCOMPLY OF THE FORM TO SEEM TO BE ACTIVE (BY SIMILARITY).

**INCOMPLY OF THE FORM TO SEEM TO BE PRODUCED BY ALTERNATIVE PRODUCED.
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-i- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTECLYTIC CLEAVAGE (BY
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PTM: PROTECLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                     SECUTENCE OF 150-756 FROM N.A. (ISOFORMS DON-1M AND DON-1S).
TISSUE-Choroid plexus;
MEDLINE-97342638; PubMed-9199335;
Busfield S.J., Michnick D.A., Chickering T.W., Revett T.L., Ma J., Woolf E.A., Comrack C.A., Dussault B.J., Woolf U., Goodearl A.D.J., Gearing D.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: HIGHEST EXPRESSION IN THE BRAIN, WITH LOWER LEVELS IN THE LUNG. IN THE CEREBELLUM, FOUND IN GRANULE AND PURKINJE CELLS.
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NEUREGULIN-2.
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INTERNAL SIGNAL SEQUENCE (POTENTIAL).
                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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-!- SIMILARITY; CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY; BELONGS TO THE NEUREGULIN FAMILY.
                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS NRG2-5; NRG2-10 AND NRG2-16A).
STRAIN=C57BL/6; TISSUE-Brain;
MEDLINE=97311398; PubMed=9168115;
Carraway K.L. III., Weber J.L., Unger M.J., Ledesma J., Yu N.,
Gassmann M., Lail.,
"Neuregulin-2, a new ligand of ErbB3/ErbB4-receptor tyrosine"
(Divergent of neuregulin 1) (DON-1)]
                                                                                                                                                                                                                                                                                                      Nature 387:512-516(1997)
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756
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                                             Mus musculus (Mouse)
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                                                                                                        NCBI_TaxID=10090;
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Pro-neuregulin-2 precursor (Pro-NRG2) [Contains: Neuregulin-2 (NRG-2)
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Pred. No. 2.6;
1; Mismatches 1; Indels
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                                           CALCIUM-BINDING.
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Q -> D (IN REF. 2).
C -> R (IN REF. 2).
MW; F09716FA7778D459 CRC64;
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MISSING (IN ISOFORM V2).
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MISSING (IN REF. 2).
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BY
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3100 CVPGYSGDRC 3109
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EMBL; U04842; AAB60436.1; -. EMBL; X12748; CAA31241.1; -.
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SMART; SM00001; EGF_like; 6.
SMART; SM00135; LY; 8.
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N-LINKED (GLCNAC. . . ) (POTENTIAL).

C -> G (IN ISOPORM NRG2-10).

WISSTROG. (IN ISOPORM NRG2-10).

WGYTGDRCQOFAMWNESKHLGFELKEABELYOKRVLTITGI
                                                                                                                                                              MISSING (IN ISOFORM DON-15).
VPGTGDRCQOPANWYRSKHGGFELKE -> NGFFGGRCLEK
LPLRLYMPDPKQK (IN ISOFORM DON-1M).
51D85DC918BE678E CRC64;
                                                                                                                                             CVALLVVG -> NGFFGQRCLEKLPLRLYMPDPKQSVLWDT
PGTGVSSSQWSTSPSTLDLN (IN ISOFORM DON-1S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 974-1021.

MEDLINE-86681810; PubMed=3000782;
Simpson R.J., Smith J.A., Moritz R.L., O'Hare M.J., Rudland P.S.,
Moritson J.R., illoyd C.J., Grego B., Burgess A.W., Nice E.C.;
"Rat epidermal growth factor: complete amino acid sequence. Homology with the corresponding murine and human proteins; isolation of a form truncated at both ends with full in vitro biological activity.";
Eur. J. Blochem. 153:629-637(1985).
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Kidney,
MEDLINE-92398779; PubMed=1524680;
Price P.M., Saggi S.J., Safirstein R.;
"Cloning and sequencing of the rat preproepidermal growth factor cDNA: comparison with mouse and human sequences.";
DNA Cell Biol. 11:481-487(1992).
                                                                                                                                                                                                                                                                                                                        01-APR-1988 (Rel. 07, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pro-epidermal growth factor precursor (EGF) [Contains: Epidermal growth factor]
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                         Score 44; DB 1; Length 756;
Pred. No. 2.1;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Price P.M.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
 CYTOPLASMIC (POTENTIAL).
            IG-LIKE C2-TYPE DOMAIN SER/THR-RICH.
                                                                                                                                                                                                                                                                                                         PRT; 1133 AA
                            EGF-LIKE.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 994-1108 FROM N.A. STRAIN-Spraque-Dawley; TISSUE-Kidney; MEDLINE-89016634; PubMed-3262867; DOTOW D.S., SIMPSON R.J.;
                                                                                                                                                                                        756 AA; 82213 MW;
                                                                                                                                                                                                        81.5%;
                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                         STANDARD;
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280 CPVGYTGDRC 289
                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                               756
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Asx_hydroxyl. EGF-like.

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| R SMART; SM00014; Link; 2.
| R SMART; SM00004; CLECT; 1.
| R SMART; SM00001; EGF_1ike; 1.
| R SMART; SM00001; EGF_1ike; 1.
| R RASITE; SM0001; EGF_1ike; 1.
| R PROSITE; PS00010; ASX_HYDROXXL; 1.
| R PROSITE; PS01186; EGF_2; 1.
| R PROSITE; PS01187; EGF_CA; 1.
| R PROSITE; PS01241; LINK; 1.
| R PROSITE; PS0041; C_TYPE_LECTIN_1; PARTIAL.
| R PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
| R PROSITE; PS0041; C_TYPE_LECTIN_3; REPEBAT; I.
| R PROSITE; PS0041; C_TYPE_LECTIN_3; REPEBAT; I.
| R PROSITE; PS0041; C_TYPE_LECTIN_3; REPEBAT; I.
           InterPro; IPPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_2.
InterPro; IPR001438; EGF_II:
InterPro; IPR0001304; Lectin_C.
InterPro; IPR000538; Link.
PRINTS; PR00010; EGFBLOOD.
InterPro; IPR000152;
                                                                                                                                                                                                                                                                                                                                    233
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P01133;
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-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
-!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                     PGCV_MACNE STANDARD; PRT; 862 AA.
028858; 028859; 028860;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Versican core protein (Large fibroblast proteoglycan) (Chondroitin sulfate proteoglycan core protein 2) (Fragments).
                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca nemestrina (Pig-tailed macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                  (POTENTIAL)
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SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                 Score 44; DB 1; Length 1133;
Pred. No. 3.1;
2; Mismatches 1; Indels
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MW; C224A302E9578031 CRC64;
                                                         N-LINKED GECNAC...)
N-LINKED GECNAC...)
N-LINKED GECNAC...)
N-LINKED GECNAC...)
C-NV GECNAC...)
C-NV (IN REF. 4).
                                                (GLCNAC
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                                                N-LINKED
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                                                                                                                                                                                   81.5%;
70.0%;
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                                                                                                                                                                                              Local Similarity 70.0
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1006 CVIGYIGERC 1015
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                                                                                                                                                                                                                                    1 CVIGXSGDRC 10
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PGCV_MACNE
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GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN,
SIMILAR TO CHONDROITIN SULFATE ATTACHMENT
SITE IN COLLAGEN TYPE IX (BY SIMILARITY).
LINK 1.
LINK 2.
GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
                                                                                                                                                                                                                                                                                                                                    CALCIUM-BINDING (POTENTIAL).
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GGCCNAC. ) (POTENTIAL).
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13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pro-epidermal growth factor precursor (EGF) [Contains: Epidermal growth factor (Urogastrone)].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95583 MW; A5D5F6153A74BB39 CRC64;
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BY SIM
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EGF-LIKE 2, CA
C-TYPE LECTIN.
                                                                                                         DOMAIN).
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744 CVPGYSGDQC 753
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ID EGF_H
AC P0113
DT 21-JU
DT 13-AU
DT 16-OC
DE Pro-e
DE Growt
GN EGF.
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EGF-LIKE 1.
EGF-LIKE 2. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 7. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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P13611; P2074; Q9URM5; Q13010; Q13189; Q15123;
Q1-JAN-1990 (Rel. 13, Created)
O1-JAN-1997 (Rel. 35, Last sequence update)
16-QCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
(Chondroitin sulfate protecoglycan core protein protecoglycan)
(Chondroitin sulfate protecoglycan core protein 2) (FG-M) (Glial
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                 CYTOPLASMIC (POTENTIAL)
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ID PGCV_HI
AC P13611;
DT 01-0AN;
DT 01-NOV;
DT 16-CCT;
DE VERSICE
DE (Chond)
DE hyalur;
GN CSPG2.
GN GS HOMO SK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOME
                                                                                                                                                                                                                                                                                             MEDLINE-89391964; PubMed-2789514; Furuya M., Akashi S., Hirayama K.; Thruya M., Akashi S., Hirayama K.; The primary structure of human EGF produced by genetic engineering, studied by high-performance tandem mass spectrometry."; Blochem. Biophys. Res. Commun. 163:1100-1106(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00010; ASK_HYDROXYL; 3.
PROSITE; PS01021; EGF_1; 1.
PROSITE; PS01186; EGF_2; 7.
PROSITE; PS01187; EGF_2; 7.
EGF_1; 1.
EGF_2; 3.
EGF_1ike domain; Repeat; Growth factor; Transmembrane; Glycoprotein;
                                                                                                             Bell G.I., Fong N.M., Stempien M.M., Wormsted M.A., Caput D., Ku L., Urdea M.S., Rall L.B., Sanchez-Pescador R.; "Human epidermal/growth factor precursor: cDNA sequence, expression in vitro and gene organization.";
Nucleic Acids Res. 14:8427-8446(1986).
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92395667; PubMed=1522591;
MEDLINE-92395667; PubMed=1522591;
Hommel U., Harvey T.S., Driscoll P.C., Campbell I.D.;
Human epidermal growth factor. High resolution solution structure and comparison with human transferming growth factor alpha.";
J. Mol. Biol. 227:271-282(1992).
I. FUNCTION: THE GROWTH FACTOR STIMULATES THE GROWTH OF VARIOUS EPIDERMAL AND EPITHELIAL TISSUES IN VIVO AND IN VITRO AND OF SO FIBEDBLASTS IN CELL CULTURE.
I. SUBCELLUIAR LOCATION: Type I membrane protein.
I. SUBCELLUIAR LOCATION: Type I membrane protein.
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO-EPIDERMAL GROWTH FACTOR.
EPIDERMAL GROWTH FACTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                              SEQUENCE OF 971-1023.
MEDLINE-77117897; Pubmed-300079;
Gregory H., Preston B.M.;
"The primary structure of human urogastrone.";
Int. J. Pept. Protein Res. 9:107-118(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR00152; Asx_hydroxyl.
InterPro; IPR00155; Egr-like.
InterPro; IPR001336; Egr-like.
InterPro; IPR001831; Egr_l.
InterPro; IPR001831; Ldl_receptor_rep.
Pfam; PF00008; Egr; 9.
Pfam; PF00008; Egr; 9.
PRINTS; PR00009; Egrcpt.
SMART; SM00179; Egr_CA.
SMART; SM00135; LX; 8.
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                                                                 SEQUENCE FROM N.A.
TISSUE=Kidney;
MEDLINE=87066721; PubMed=3491360;
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HSSP; P01132; 1EGF.
Genew; HGNC:3229; EGF.
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sapiens (Human)
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                                          NCBI_TaxID=9606;
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DOMAIN
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SIGNAL
 "Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chromosome 5 (5q12-5q14)."; Genomics 14:845-851(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zako M., Shinomura T., Ujita M., Ito K., Kimata K.; "Expression of PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-9613482; PubMed-9627343;
Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;
"Differential expression of versican isoforms in brain tumors.";
J. Neuropathol. Exp. Neurol. 55:528-533(1996).
-i. FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in
                                                                                                                                                                                                                                                                                                                                           Krusius T., Gehlsen K.R., Ruoslahti E.;
"A fibroblast chondroitin sulfate proteoglycan core protein contains
lectin-like and growth factor-like sequences.";
J. Biol. Chem. 262:13120-13125(1987).
                                                                                                                                                                  Multiple domains of the large fibroblast proteoglycan, versican.";
                                                         Naso M.F., Zimmermann D.R., Iozzo R.V.;
Characterization of the complete genomic structure of the human
versican gene and functional analysis of its promoter.";
J. Biol. Chem. 269:32999-33008(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lemire J.M., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.,
                                                                                                                                                                                                                                           Dours-Zimmermann M.T., Zimmermann D.R.;
"A novel glycosaninoglycan attachment domain identified in two
alternative splice variants of human versican.";
J. Biol. Chem. 269:32992-32998(1994).
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Versican/PG-M isoforms in vascular smooth muscle cells.";
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perides G., Lane W.S., Andrews D., Dahl D., Bignami A., "Isolation and partial characterization of a glial hyaluronate-binding protein."; J. Biol. Chem. 264:5981-5987(1989).
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 251-347 FROM N.A.
MEDILINE-93122792; PubMed=1478664;
ICAZO R.V., Naso M.F., Cannizzaro L.A., Wasmuth J.J.,
McPherson J.D.;
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MEDLINE-99327053; PubMed=10397680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89174663; PubMed-2466833;
                                  SEQUENCE FROM N.A. (ISOFORM VO).
MEDLINE-95105188; Pubmed=7528742;
                                                                                                                                 TISSUE-Placenta;
MEDLINE-90059882; PubMed-2583089;
Zimmermann D.R., Ruoslahti E.;
                                                                                                                                                                                                                     TISSUE-Glial tumor;
MEDLINE-95105187; PubMed-7806529;
                                                                                                                                                                                                                                                                                                                     TISSUE-Lung fibroblast;
MEDLINE-88007514; PubMed-2820964;
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                                                                                                                                                                                  EMBO J. 8:2975-2981(1989).
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           WCBI_TaxID=9606;
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regulation of cell motility, growth and differentiation. Binds
                                                                  SUBCELLUIAR LOCATION: Secreted; extracellular matrix.
STRERMATIVE PRODUCTS: At least 5 isoforms; V0 (shown here), V1,
V2, V3 and Vint; are produced by alternative splicing.
TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expressed
in normal brain, gliomas, medulloblastomas, schwannomas,
neurofibromas, and menniglomas; v2 is restricted to normal brain
and gliomas; v3 is found in all these tissues except
                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 LINK DOMAINS.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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R SMART; SM00032; CLECT; 1.

R SMART; SM00034; CLECT; 1.

R SMART; SM00001; EGF_11ke; 1.

R SMART; SM00001; EGF_11ke; 1.

R SMART; SM00445; LINK; 2.

R PROSITE; PS00010; ASX_HYDROXYL; 1.

R PROSITE; PS01186; EGF_2; 1.

R PROSITE; PS01187; EGF_2; 1.

R PROSITE; PS01187; EGF_A; 1.

R PROSITE; PS01041; CLYPE_LECTIN_1; 1.

R PROSITE; PS00415; CTYPE_LECTIN_1; 1.

R PROSITE; PS00415; CTYPE_LECTIN_2; 1.

R PROSITE; PS0041; CTYPE_LECTIN_1; 1.

R PROSITE; PS0041; CTYPE_LECTIN_1; 1.

R PROSITE; PS0041; CTYPE_LECTIN_1; 1.

R PROSITE; PS0041; CTYPE_LECTIN_2; 1.

R PROSITE; PS0041; CTYPE_LECTIN_3; 1.
                                                                                                                                                                                                                                                                                                                                         meduiloblastomas.
DEVELOPMENTAL STAGE: Disappears after the cartilage development.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000761; EGF-like.
InterPro; IPR0010438; EGF_C.
InterPro; IPR001438; EGF_C.
InterPro; IPR00159; IG.
InterPro; IPR001509; IG.
InterPro; IPR001504; Lectin_C.
InterPro; IPR000508; Ink.
InterPro; IPR000508; Link.
InterPro; IPR000508; Link.
InterPro; IPR000508; Sushi_SCR_CCP.
Pfam; PP000047; IG; I.
Pfam; PP00084; Sushi; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U16306; AAA65018.1; -. EMBL; X15998; CAA34128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U26555; AAA67565.1; -. D32039; BAA06801.1; -. J02814; AAA36437.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S52488; AAB24878.1; -.
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PIR; A29348; A29348.
PIR; A30358; A30358.
HSSP; P01132; IEGF.
Genew; HGNC:2464; CSPG2.
                                           hyaluronic acid.
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EMBL;
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                                                                                                                                                                                                                                                                                                                            EMBL; AF229448; AAL08213.1; ---

BERL; AF229448; AAL08213.1; ---

BERL; CDB-CENE-C11128-2; JAG1.

RINTEPTO; IPR001774; DSL.

RINTEPTO; IPR000174; DSL.

RINTEPTO; IPR000142; BGF-2.

RINTEPTO; IPR00048; BGF-2.

REF ARM; PF00008; BGF, 18.

REF ARM; PF000010; ASK, HYDROXYL; 9.

REF ARM; PF000010; ASK, HYDROXYL; 9.

REF ARM; PROSTITE; PS01186; BGF-2; 12.

REF ARM; PROSTITE; PS01186; BGF-2; 12.

REF ARM; REF ARM; BGF-2; 13.

REF ARM; REF ARM; BGF-1; ARM; BF00TENTIAL.

REPORT TRANSHENDER SIGNAL.

REF TRANSHENDER SIGNAL.

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EGF-LIKE 2.

EGF-LIKE 3.

EGF-LIKE 3.

EGF-LIKE 5.

EGF-LIKE 6.

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EGF-LIKE 7.

EGF-LIKE 10.

EGF-LIKE 10.

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EGF-LIKE 14.

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EGF-LIKE 19.

EGF-LIKE 19.

EGF-LIKE 11.

EGF-LIKE 1
        FUNCTION: Ligand for multiple Notch receptors and involved in the mediation of Notch signaling (By similarity). Seems to be involved in cell-fate decisions.
SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 DSL DOMAIN.
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CYTOPLASMIC (POTENTIAL).
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                                                                   LINK 2.
GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
                                                                                                                                                                            CALCIUM-BINDING (POTENTIAL)
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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"Isolation, characterization and expression analysis of Zebrafish
Jagged genes.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .) (POTENTIAL)
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EGF-LIKE 2, CAL
C-TYPE LECTIN.
SUSHI.
BY SIMILARITY
BY SIMIL
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Pred. No. 14;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                         embryo.";
Dev. Biol. 146:89-99(1991).
-!- FUNCTION: FORM THE APICAL LAMINA, A COMPONENT OF THE EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: MODERATE LEVELS IN UNFERTILIZED EGGS AND DURING EARLY CLEAVAGE, THEN RAPLOLY INCREASES IN ABUNDANCE BETWEEN LATE MORULA AND MESRICHYME BLASTULA STAGES TO MAXIMAL LEVELS MAINTAINED THROUGH SUBSEQUENT STAGES. EXPRESSED BOTH MATERNALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: EXTRACELLULAR. IN VESICLES IN THE CYTOPLASM OF UNFERTILIZED EGGS, THEN TO THE BASE OF THE HYALIN LAYER THROUGHOUT DEVELOPMENT AND FINALLY IN THE APICAL LAMINA IN LATE
                                                                                       MEDLINE-89196806; PubMed-2784773;
Hunt L.T., Barker W.C.;
"Avidin-like domain in an epidermal growth factor homolog from a sea
                                                                                                                                                                                                                                                            CHARACTERIZATION.
MEDILINE-91285254; PubMed-2060714;
Bisprove B.W., Andrews M.E., Raff R.A.;
Bisprove B.W., products of an EGF repeat-containing gene, form a unique extracellular matrix structure that surrounds the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBRYOS AND EARLY LARVAE.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; IA (SHOWN HERE) AND IB; ARE
PRODUCED BY ALTERNATIVE SPLICING. THE SMALL FORM (IB) LACKS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 21 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 1 CUB DOMAIN. SIMILARITY: THE C-TERMINAL DOMAIN OF THIS PROTEIN IS SIMILAR TO AVIDIN/STREPTAVIDIN.
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SMART; SM00179; EGF_CA; 18.
SMART; SM001019; EGF_L1ke; 3.
PROSITE; PS00010; ASYLPROXYL; 19.
PROSITE; PS00022; EGF_1; 19.
PROSITE; PS0180; CUB; 1.
PROSITE; PS01180; EGF_2; 19.
PROSITE; PS01180; EGF_2; 19.
BROSITE; PS01187; EGF_CA; 18.
Biotin; Alternative splicing; EGF-like domain; Repeat; Signal;
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InterPro; IRR000899; CUB_domain.
InterPro; IRR000561; EGF-11ke.
InterPro; IRR001801; EGF_Z.
InterPro; IRR00181; EGF_II.
InterPro; IRR001818; EGF_II.
InterPro; IRR00199; Laminin_EGF.
Pfam; PF00008; EGF; 21.
Pfam; PF0011382; Avidin; 1.
PRINTS; PR00011; EGFLAMININ.
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InterPro; IPR000088; Avidin.
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EMBL; X17530; CAA35571.1; --
EMBL; M17421; AAA30050.1; --
EMBL; M17421; AAA30050.1; --
EMBL; A27533; CAA35573.1; --
PIN; A29316; A29316.
      Science 237:1487-1490(1987)
                                                                                                                                                                                                   FASEB J. 3:1760-1764(1989)
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                                                               AVIDIN-LIKE DOMAIN.
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      MANA WARANA WARA
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
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MEDLINE-90112459; PubMed=2514273;
Delgadillo-Reynoso M.G., Rollo D.R., Hursh D.A., Raff R.A.;
"Structural analysis of the uBGF gene in the sea urchin strongylocentrotus purpuratus reveals more similarity to vertebrate than to invertebrate genes with EGF-like repeats.";
J. Mol. Evol. 29:314-327(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-FBE-1966 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibropellin I precursor (Epidermal growth factor-related protein 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .) (POTENTIAL)
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Pred. No. 8;
2; Mismatches
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BY SIMILAN
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60.0%;
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1242 AA;
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NCBI_TaxID=7668;
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PubMed=10790539;
Formstone C.J., Barclay J., Rees M., Little P.F.R.;
"Chromosomal localization of Celsr2 and Celsr3 in the mouse; Celsr3 is
a candidate for the tippy (Lip) lethal mutant on chromosome 9.";
Mamm. Genome 11:392-394(2000).
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SEQUENCE FROM N.A.
MEDLINE=99418630; PubMed=10490098;
Usul T., Shima Y., Shimada Y., Hirano S., Burgess R.W., Schwarz T.L.,
Takeichi M., Uemura T.;
"Flamingo, a seven-pass transmembrane cadherin, regulates planar cell
polarity under the control of frizzled.";
cell 98:585-595(1999).
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 2 precursor (Flamingo 1)
BY SIMILARITY.
BY SIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10090;
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Pred. No. 10;
2; Mismatches 2; Indels
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SEQUENCE OF 1913-2796 FROM N.A., AND TISSUE SPECIFICITY
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316 CPLGFSGDNC 325
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Strausberg R.;
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PubMed=11850187;
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Best Local Similarity
Matches 6; Conserv
       CLR2_MOUSE
ID CLR2_MOUSE
     DISULETO
CARBOHYO
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SEQUENCE
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CELSR2.
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Mech. De
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EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 20.

EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).
                                                 FIBROPELLIN I.
EGF-LIKE 1.
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BY SIMILARITY.
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  Calcium-binding.
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PROSITE; PS50221; GPS; 1.

PROSITE; PS50025; LAM_G_DOMAIN; 2.

G-protein coupled receptor; Transmembrane; Glycoprotein;

EGF-11ke domain; Calcium-binding; Laminin EGF-11ke domain; Repeat;

Developmental protein; Hydroxylation; Signal.

SIGNAL
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N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                CADHERIN EGF LAG SEVEN-PASS G-TYPE RECEPTOR 2.
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CALIKE 1, CALCIUM-BINDING.
LAMININ G-LIKE 1.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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               signaling during nervous system formation.

Signaling during nervous system formation.

SIGNELLIAR LOCATION: Integral membrane protein.

SIGNELLIAR LOCATION: Integral membrane protein the developing CNS, expression is uniform along the rostrocaudal axis. During gastrulation, it is expressed within the anterior neural ectoderm. At E10, expression is strong in the ventricular zones (WZ) in all sectors of the brain, and lower in the marginal zones (WZ) in all sectors of the brain, and lower in the marginal zones (WZ) in all sectors of the brain, and lower in the marginal zones (WZ).

Sectors of the brain, and lower in the marginal zones (WZ) in all sectors of the brain, and lower in the cerebral with the present in the brain. It is strong in VZ, lower in MZ, except in the cerebral with the ferenciating fields than in VZ, except in the cerebral hemispheres, and to a lesser extent in the tectum and cerebral hemispheres, and to a lesser extent in the fetal lungs, kidney and epithelial in the newborn and postruatal stages, expression remains restricted to the VZ as well as in migrating and postmigratory cells throughout the brain.

SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.

SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 GAS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAD; MCI 1898235; Celsr2.
InterPro; IPR000125; Asx_hydroxyl.
InterPro; IPR000125; Celsr2.
InterPro; IPR000125; EGF_2.
InterPro; IPR000132; EGF_2.
InterPro; IPR000132; EGF_2.
InterPro; IPR000142; EGF_2.
InterPro; IPR001093; Dormn_receptor.
InterPro; IPR001093; Dormn_receptor.
InterPro; IPR001094; Laminin_GF.
InterPro; IPR001093; PRD_cys_rich.
Pfam; PF00002; 7tn_2; 1.
Pfam; PF00003; 7tn_2; 1.
Pfam; PF00008; EGF; 5.
Pfam; PF00008; EGF; 5.
Pfam; PF00018; EGF; 5.
Pfam; PF00008; EGF; 5.
Pfam; PF00009; EGF_15.
Pfam; PF00009; EGF_16.
PRINTS; PR0011; EGFLAMININ.
PRINTS; PR0011; EGFLAMININ.
PRINTS; PR0011; EGF_1ke; 6.
SWART; SW00118; EGF_1ke; 6.
SWART; SW00008; HORTMR; 1.
SWART; SW00008; GAPERIN. 1; 6.
SWART; SW00008; GAPERIN. 1; 6.
PROSITE; PS00022; EGF_1; 6.
PROSITE; PS00022; EGF_1; 6.
PROSITE; PS00049; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
PROSITE; PS00186; EGF_2; 2.
PROSITE; PS00186; EGF_2; 3.
PROSITE; PS00186; EGF_2; 4.
PROSITE; PS00186; EGF_2; 5.
PROSITE; PS00186; EGF_2; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB028499; BAA84070.1; -. BMBL; AR011573; AAC68837.1; -. EMBL; BC005499; AAH05499.1; -. HSSP; P00740; 1EDM.
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Matches

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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-VC-16 / DSW 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., Mockenbey K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., Weidman J.F., McDonald L., Utterback A., Soverbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Badow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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0
                                                                                Score 40; DB 1; Length 53;
Pred. No. 0.79;
2; Mismatches 2; Indels
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Pred. No. 0.85;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 protein; Complete proteome.
57 AA; 6885 MW; 4C71BDEB722568B8 CRC64;
                                            74F615B4A05774D4
                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF0402.
        BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTC2_MOUSE STANDARD; PRT; 2470 AA 035516; Q60941; Q06008; Created) 15-7UN-2002 (Rel. 41, Created) 15-7UN-2002 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001076; AAB90836.1; -.
                                                                                74.1%;
60.0%;
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50.0%;
                                            6149 MW;
                                                                                                     Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 74.1
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                   STANDARD;
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33 CVFGYVGERC 42
                                                                                                                                                               1 CVIGXSGDRC 10
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23 CIMGYTGKRC 32
        33
53
53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2234;
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029845;
                          NON_TER
SEQUENCE
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        DISULFID
                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Mol. Endocrinol. 6:63-70(1991).
-!- FUNCTION: THE GROWTH FACTOR STIMULATES THE GROWTH OF VARIOUS
EPIDERWAL AND EPITHELIAL TISSUES IN VIVO AND IN VITRO AND OF SOME
FIBROBLASTS IN CELL CULTURE.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91197366; Pubmed=2015058;
Pascall J.C., Jones D.S.C., Doel S.M., Clements J.M., Hunter M.,
Fallon T., Edwards M., Brown K.D.;
"Cloning and characterization of a gene encoding pig epidermal growth
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                   Score 41; DB 1; Length 2920;
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                -> L (IN REF. 3).
-> V (IN REF. 3).
-> R (IN REF. 1).
-> R (IN REF. 2).
-> S (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last annotation update)
Epidermal growth factor (EGF) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 AA
                                                                                                                                                                                                                                                                                                                                     Pred. No. 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
EGF-like domain; Growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINEARY; PUL132; IEGF.
InterPro; IPRO00561; EGF-like.
Pfam; PF00008; EGF; I.
                                                                                                                                                                                                                                                                                                               75.98;
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                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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2025
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2062
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2334
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20
31
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  1502
11566
11742
11828
11901
12025
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PEPTIDE
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Gaps

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MEDLINE=21374376; PubMed=11459941;
Tonservation of the biochemical mechanisms of signal transduction among mammalian Notch family members.";
Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
I. FONCTION: Functions as a receptor for membrane-bound ligands agged1, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus.
Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May play an essential role in specification and/or differentiation.

Specification and/or differentiation.

C. SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
MEDLINE-95333893; PubMed-7609614;
Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Tsujimoto Y.;
"Differential expression of Notchi and Notch2 in developing and adult
    15-JUN-2002 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mutation in ankyrin repeats of the mouse Notch2 gene induces early
                                                                                                                                                                                                    STRAIN-C57BL/6; TISSUE-Thymus;
Hamada Y., Higuchi M., Tsujimoto Y.;
Complete amino acid sequence and mutliform transcripts encoded by
single copy of mouse Notch2 gene.";
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D., Martin D.I.,
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                     ø
                                                                                                                                                                                                                                                                                                                                                                                         Lardelli M., Lendahl U.; "Motch A and Motch B-two mouse Notch homologues coexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699 MEDLINE-21523956; Pubmed-11518718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.; "Murine notch homologs (N1-4) undergo presenilin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin D.I.;
"Inhibition of granulocytic differentiation by mNotchl.";
Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99396706; PubMed~10393120;
Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R.,
Tsujimoto Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Res. Mol. Brain Res. 29:263-272(1995),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 276:40268-40273(2001).
                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6 X CBA; TISSUE-Embryo;
MEDLINE-93178563; PubMed-8440332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1765-2153 FROM N.A.
MEDLINE-97075110; PubMed-8917536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell Res. 204:364-372(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 embryonic lethality.";
Development 126:3415-3424(1999).
                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 316-1518 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     variety of tissues."
15-JUN-2002 (Rel. 41,
                                                                               Mus musculus (Mouse).
                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                              NOTCH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 2. NOTCH EXTRACELLULAR TRUNCATION. NOTCH INTRACELLULAR DOMAIN.
           produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in the brain, liver, kidney, neuroepithelia, somites, optic vesicles and branchial arches, but
                                                                  DEVELOPMENTAL STAGE: Expressed in the embryonic ventricular zone,
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50088 ANK_REPEAT; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS500101, ASX_HYDROXYL; 22.
PROSITE; PS001022; EGF_1; 33.
PROSITE; PS01186; EGF_2; 27.
PROSITE; PS01187; EGF_CA; 22.
PROSITE; PS01187; EGF_CA; 22.
PROSITE; PS01187; EGF_CA; 22.
PROSITE; PS01187; EGF_CA; 22.
PROSITE; PS01187; EGF_CA; 23.
PROSITE; PS01187; EGF_CA; 24.
PROSITE; PS01187; EGF_CA; 25.
PROSITE; PS01187; EGF_1; S10181; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1.
EGF-LIKE 2.
                                                                                                                                                                                                                                                          -i- PTM: Phosphorylated.
-i- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
-i- SIMILARITY: CONTAINS 34.5 EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 2 LIN/NOTCH REPEATS.
-i- SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002110; ANK.
InterPro; IPR001512; Asx.hydroxyl.
InterPro; IPR000151; BGF-1ike.
InterPro; IPR001681; EGF-2.
InterPro; IPR001881; EGF_2.
InterPro; IPR001881; EGF_1.
InterPro; IPR001881; EGF_1.
InterPro; IPR001680; Notch.
Pfam; PF00008; EGF; 35.
Pfam; PF00006; notch; 2.
PRINTS; PR00010; EGFBLOD.
PRINTS; PR001452; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SM00248; ANK; 4.
SWART; SM00179; EGF_CA; 22.
SWART; SM00001; EGF_11ke; 12.
SWART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D32210; BAA22094.1; -. EMBL; X68279; CAA48340.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U31881; AAC52924.1; -. P16109; 1FSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:97364; Notch2.
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1677
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1678
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PAGESTATION PROCESSING.

RA BLAUMHOLIP PROCESSING.

RA BLAUMHOLIPE C.M. Ol H. Zagouras P., Artavanis-Tsakonas S.;

RA BLAUMHOLIPE C.M. Ol H. Zagouras P., Artavanis-Tsakonas S.;

RE TINTRACEDIULAT CLEANDS.

RE THE PLASMA MEMDIANDS.

RE THE PLASMA MEMBRATORY TO THE PLASMA S.

REDINING-99180765; PubMed-10079256;

RA GAY G.E., Mann R.S., Matsadis E., Henrique D., Carcangiu M.-L.,

RATO. I.S., Matsadis E., Henrique D., Carcangiu M.-L.,

REDALING-99180765; PubMed-10079256;

REDALING-9918076; PubMed-1007926;

REDALING-9918076;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stifani S., Blaumueller C.M., Redhead N.J., Hill R.E., Artavanis-Tsakonas S.; "Human homologs of a Drosophila enhancer of split gene product define a novel family of nuclear proteins.";
                                                                                                                                                                                                                                                                                                                          Lemasson I., Devaux C., Mesnard J.M.; "Partial sequence of EGF-like repeat domain of human Notch2 mRNA."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      Correa R.G., Camargo A.A., Moreira E.S., Simpson A.J., "Human Notch2, a novel member of cell-fate determining NOTCH
                                                                                              "Complete human notch 2 (hN2) cDNA sequence.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                              Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
MEDLINE-93265135; PubMed-1303260;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1810-2447 FROM N.A.
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                                                                 Blaumueller C.M., Mann R.S.;
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Nat. Genet. 2:119-127(1992).
                                                                                            "Complete human notch 2
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0404721; 09H240; 099734;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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EGF-LIKE 5. CALCIUM-BINDING (PC EGF-LIKE 6. (INCOMPLETE).

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CYTOPLASMIC (POTENTIAL).

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PROSITE; PS50297; ANK_REPEAT; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS00010; ASX_HYDROXYL; 22.
PROSITE; PS00186; EGF_1; 34.
PROSITE; PS01186; EGF_2; 29.
PROSITE; PS01187; EGF_CA; 22.
Receptor; Transcription regulation; Activator; Differentiation; Developmental protein; Repeat; ANK repeat; EGF-like domain; Transmembrane; Glycoprotein; Signal; Phosphorylation.
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InterPro; IPR001881; EGF_Ca.
InterPro; IPR001439; EGF_II.
InterPro; IPR001499; Laminin_EGF.
InterPro; IPR000160; Notch.
Pfam; PF00008; EGF; 35.
Pfam; PF00006; EGF, 35.
PRINTS; PR00010; EGFBLCOD.
PRINTS; PR00011; EGFBLCOD.
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SMART; SM00179; EGF_CA; 22.
SNART; SM000179; EGF_CA; 22.
SNART; SM000179; EGF_Like; 12.
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EGF-like.
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99nfs9 drosophila

996kg6 homo sapien

996kg6 homo sapien

995nd4 felis silve

99bdq0 sus scrofa

99bdq0 sus scrofa

99bdq0 canis famil

99pa5 branchiosto

99w4y4 drosophila

981521 caenorhabdi

981522 caenorhabdi

981522 caenorhabdi

981523 caenorhabdi

981523 caenorhabdi

981523 caenorhabdi

981523 caenorhabdi

981523 caenorhabdi

99bw29 homo sapien

012891 homo sapien

057499 brachydanio

99pm9 caenorhabdi
                                                          035883 rattus norv
05348 rattus norv
091yfl arabidopsis
09wvb5 mus musculu
09r0m0 mus musculu
09r0m0 ara musculu
090891 caenorhabdi
022913 caenorhabdi
                              035452 mus musculu
054796 mus musculu
061240 halocynthia
                ytechinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberger, Strausberger, Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC017681; AAM17681.1; EMBL; BC017681; AAM17681.1; EMBL; BC017681; AAM17681.1; EMBL; BC00135; ASX_bydroxyl.

R InterPro; IPR000135; BGF_18.

R InterPro; IPR001881; BGF_Ca.

R InterPro; IPR001881; BGF_Ca.

R InterPro; IPR001881; BGF_Ca.

R Pfam; PF00008; BGF; 8.

R Pfam; PF00008; BGF; 9.

R SMART; SM00118; BGF; 9.

R SMART; SM00118; BGF. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_3.

PROSITE; PS00022; EGF_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_6.

PROSITE; PS01187; EGF_CA; UNKNOWN_6.

SEQUENCE 1200 AA; 131317 WW; BGA44F7294746476 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8VD07;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to epidermal growth factor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1200 AA
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               016004
035452
054796
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Q9LYF1
Q9WVB5
Q9R0M0
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Q9GPM9
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Q8STG0
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09BEA0
09GPA5
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Q95ND4
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Best Local Similarity 90.00,
                                                                                              PRELIMINARY;
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TISSUE-KIDNEY;
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Q28867 equus cabal
Q20043 caenorhabdi
Q90xx0 orectolobus
Q8wtp0 halocynthia
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homo sapien
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                                                                                                                              (without alignments)
49.850 Million cell updates/sec
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                                                                                                           July 2, 2003, 07:25:01; Search time 41.3333 Seconds
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               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q9VC97
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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sp_bacteria:*
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54
1 CVIGXSGDRC 10
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sp_rodent:*
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Match Length DB
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sp_mhc:*
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Q9UN94
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Tandell M.D., Zhang O., Chen Lix.,
RA Britl J.F., Appayani A., An H.-J., Andrews-Pennikoh C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Barendale J., Bayerktaroglu L., Basaley E.M.,
Ballew R.M., Basu A., Barendale J., Bayerktaroglu L., Basaley E.M.,
Ballew R.M., Basu A., Barendale J., Bayerktaroglu L., Basaley E.M.,
Beson R.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Grenson R., Doup L.B., Downes M.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek B., Delcher A., Donnes C., Perraz C., Ferriera S., Fleischman W.,
RA Glodek B., Doup L.B., Downes M. Dugan-Rocha S., Fleischman W.,
RA Hartis N.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,
RA Hartis N.L., Harvey D., Helman T.J., Herandac J.R., Rock J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Rako P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,
Liako P., Lei Y., Levitsky A.A., Li J.J., Morniy L.M., Nelson D.L.,
Rako P., Lei Y., Levitsky A.A., Li J.J., Morniy D.M., Nelson D.L.,
Rabon D.R., Nolym M., Wurphy B., Murphy L., Morniy U.M., Nelson D.L.,
Rabon D.R., Nelson K.A., Nikon K., Nikon K., Nikon K., Palazzolo M., Pittamos I., Simper R., Vender E., Wang A.H., Wang X.,
Rayer Sheder K., Wassarman D.A., Weinster E., Wang A.H., Wang X.,
Rayer Sheder K., Wassarman D.A., Weinster E., Wang S., Yao Q.A.,
Rayer S., Wassarman D.A., Weinster C., Wu D., Yang S., Zhu X., Smith H.O.,
Rayer S., Ponder S., Whoodage T., Worley K., Wu D., Yang S., Zhu X., Smith H.O.,
Rayer Pondone sequence of Drosophila melanogaster.";
Rayer S., Pan
                                                                                                                                                                                                                                                                                           CRB protein.
CRB OR CG6383.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                       PRT; 2146 AA
                                                                                                                                                                                                                           Created)
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InterPro; IPR000551; EGF-like.
InterPro; IPR000561; EGF-2.
InterPro; IPR001438; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR002049; Laminin_G.
Pfam; PF000008; EGF; 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
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                         992 CVIGYSGDRC 1001
                                                                                                                                                                          PRELIMINARY;
  1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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  PRINTS; FRUCCE.
PRINTS; PROCOLI; EGFLAMININ.
SWART; SM00119; EGF_CA; 11.
SWART; SM001019; EGF_LIKe; 16.
SWART; SM00201; EGF_LIKe; 16.
SWART; SM00202; EGF_LIKe; 16.
PROSITE; PS00022; EGF_L; 25.
PROSITE; PS01187; EGF_CA; 13.
Calcium-binding; EGF-LIKe domain; Glycoprotein; Hydroxylation; Repeat.
Calcium-binding; EGF-LIKe domain; Glycoprotein; Hydroxylation; Repeat.
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MEDLINE-99335363; PubMed-10405327;
Williams S.J., Munster D.J., Quin R.J., Gotley D.C., McGuckin M.A.;
"The MUC3 gene encodes a transmembrane mucin and is alternatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                       1; Indels
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Last annotation update)
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Last annotation update)
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InterPro; IPRO00561; EGF-11ke.
SMART; SM00181; EGF-1; UNKNOWN_2.
PROSITE; PS00186; EGF_1; UNKNOWN_2.
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                                                                                                                                                                                                                                                           DB 2.2;
                                                                                                                                                                                                                                                           Score 49; DB Pred. No. 2.2; 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UN94 PRELIMINARY;
Q9UN94;
01-MAY-2000 (TrEMBLrel. 13, Cz
01-MAY-2000 (TrEMBLrel. 13, La
01-MAR-2002 (TrEMBLrel. 20, La
Mucin 3 (Fragment).
                                                                                                                                                                                                                                                           90.78;
70.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-pEC-2001 (TrEMBLrel. 19,
PRINTS; PR00010; EGFBLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                  Local Similarity 70.0
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                            569 CAVGYSGDRC 578
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14 CLPGFSGDRC 23
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InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 5.
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233 CYLGYSGDKC 242
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TISSUE=SMALL INTESTINE;
                                                                                                                                                                                                   Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
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09н306;
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RESULT 6
Q21756
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                                                             MEDLINE-99335363; PubMed=10405327; Williams S.J., Munster D.J., Quin R.J., Gotley D.C., McGuckin M.A.; Williams S.J., Munster D.J., Quin R.J., Gotley D.C., McGuckin M.A.; "The MUC3 gene encodes a transmembrane mucin and is alternatively spliced.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99335363; PubMed=10405327; Williams S.J., Munster D.J., Quin R.J., Gotley D.C., McGuckin M.A.; Williams S.J., Munster D.J., Quin R.J., Gotley D.C., McGuckin M.A.; Fire MUC3 gene encodes a transmembrane mucin and is alternatively spliced.";
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 AA; 40953 MW; 88F3F0E3F439A3C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             308 AA; 34665 MW; A5782A702D4EAE86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                        Biochem. Biophys. Res. Commun. 261:83-89(1999)
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EMBL; AF14371; AAD45882.1; -
Interpro; IPR000561; EGF-like.
Interpro; IPR000083; SEA_domain.
Ffam; PF01390; SEA; 1.
SWART; SW00181; EGF; 2.
SWART; SW0020; SEA; 1.
PROSITE; PS00022; EGF_1; UNKNOWN_2.
PROSITE; PS00186; EGF_1; UNKNOWN_2.
PROSITE; PS00186; EGF_1; UNKNOWN_2.
PROSITE; PS00186; EGF_1; UNKNOWN_3.
EGF_1ike domain; Glycoprotein.
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                                                                                                                                                                                                                                                                                                               PROSITE; PS00022; EGF_1; UNKNOWN_2. PROSITE; PS01186; EGF_2; 1. PROSITE; PS50024; SEA; 1. EGF-like domain; Glycoprotein.
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                                                                                                                                                                         EMBL; AF143372; AAD45883.1; -.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000082; SEA_domain.
FFdm; PF01390; SEA; 1.
SMART; SM00181; EGF; 1.
SMART; SM00200; SEA; 1.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2002 (TrEMBLrel. 20,
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Matches 7; Conservative
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les 7; Conservative
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14 CLPGFSGDRC 23
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14 CLPGFSGDRC 23
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                                            TISSUE-COLON MUCOSA;
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SEQUENCE
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MEDLINE-21183349; PubMed=11289722;
Kyo K., Mito T., Nagawa H., Lathrop GM., Nakamura Y.;
"Associations of distinct variants of the intestinal mucin gene MUC3A
with ulcerative colitis and Crohn's disease.";
J. Hum. Genet. 46:5-20(2001).
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                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BRISTOL N2;
Murray J., Le T.T.;
"The sequence of C. elegans cosmid R05G6.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; US8746; AAB00626.1; -.
HSSP; P01132; 1A3P.
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PROSITE; PS00022; EGF 1; UNKNOWN_7.
PROSITE; PS01186; EGF_2; 6.
EGF-1ike domain; G1ycoprotein; Hypothetical protein.
SEQUENCE 372 As; 39085 MW; DB36AB251EEB6884 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Intestinal mucin (Fragment).
                                                                      01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Hypothetical 39.1 kDa protein.
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     372 AA
Q21756 PRELIMINARY; PRT; Q21756; 01-NOV-1996 (TIEMBLE-1. 01, Last sequ 01-DEC-2001 (TIEMBLE-1. 19, Last sequ 01-DEC-2001 (TIEMBLE-1. 19, Last annotation)
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Query Match
Best Local Similarity 70.0.
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01-MAR-2001 (TrEMBLrel. 01-MAR-2001 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. MUC3B mucin (Fragment).
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Best Local Similarity 70.0
Matches 7; Conservative
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526 CLPGFSGDRC 535
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549 CLPGFSGDRC 558
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                          Query Match 81.5%; Score 44; DB 4; Length 877; Best Local Similarity 70.0%; Pred. No. 8; Matches 7; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                   PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS0024; SEA; 1.
1 1.
SEQUENCE 877 AA; 93720 MW; 09EE5E86EC838DFA CRC64;
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SEQUENCE 878 AA; 93685 MW; 1414E7E00AFE5B4C CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09H3Q7 PRELIMINARY, PRT, 878 AA. 09H3Q7, 00H3Q7, CLAMPAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) MUG3A.
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PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50024; SEA; 1.
EMBL; AB038784; BAB12118.1; -.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000082; SEA_domain.
FFam; PF01390; SEA; 1.
SMART; SM00181; EGF; 2.
SMART; SM00200; SEA; 1.
                                                                                                                                                                                                                                                       ntestinal mucin (Fragment).
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Matches 7; Conservative
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| 525 CLPGFSGDRC 534
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526 CLPGFSGDRC 535
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Q9GZZ2
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09H3Q7
ID 09H3Q
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WEDLINE-21183349; PubMed-11289722;

MEDLINE-21183349; PubMed-11289722;

MEDLINE-21183349; PubMed-11289722;

MEDLINE-21183349; PubMed-11289722;

MA Kyo K., Muto T., Magawa H., Lathrop GM., Nakamura Y.;

The Associations of distinct variants of the intestinal mucin gene MUC3A at the ulcerative colitis and Crohn's disease.";

J. Hum. Genet. 46:5-20(2001).

M. TherPro: IPR00061; EGF-11ke.

M. InterPro: IPR00062; EGF-11ke.

M. InterPro: IPR00062; EGF-11ke.

M. SMART; SM0001; EGF-11ke; 1.

M. SMART; SM0001; EGF-11ke; 1.

M. SMART; SM0001; EGF-11ke; 1.

M. SMART; SM0001; EGF-1; UNKNOWN_1.

M. PROSITE; PS01186; EGF-2; 1.

M. M. BISE9B97FIEC5795 CRC64;
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Pratt W.S., Crawley S., Hicks J., Ho J., Nash M., Kim Y.S., Gum J.R.,
Swallow D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL, AJ291390; CAC19572.1; -.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000082; SEA_domain.
Finn; PF01390; SEA; 1.
SMART; SM00181; EGF; 2.
SMART; SM00181; EGF; 2.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS50024; SEA; 1.
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Last sequence update)
Last annotation update)
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Gaps

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"Identification of the horse epidermal growth factor (EGF) coding sequence and its use in monitoring EGF gene expression in the endometrium of the pregnant mare.";

The middle of the pregnant mare.";

M. Mol. Endocrinol. 12:341-350(1994).

EMBL; S73527; AAB3226.1;

InterPro; IPR0001551; BSF-11ke.

EMBL; PR00019; EGFT.

EMBL; SM00019; EGFT.

EMBL; SM00010; EGFT.

EMBL; S
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Eukaryota: Metazoa; Chamatoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor (Fragment).
Epidermal growth factor (Fragment).
Eduus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                     Score 44; DB 4; Length 1217;
Pred. No. 11;
2; Mismatches 1; Indels
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Stewart F., Power C.A., Lennard S.N., Allen W.R., Amet L.,
Edwards R.M.;
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PROSITE; PS50024; SEA; 1.
EGF-Like domain; Glycoprotein.
NON TER
SEQUENCE 1217 AA; 129171 MW; 0783A4003C969664 CRC64;
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Pred. No. 1.1;
3; Mismatches
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                                                                                                                                                                                                              81.5%;
70.0%;
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Best Local Similarity 70.0.
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865 CLPGFSGDRC 874
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Best Local Similarity
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MEDLINE-97476275; PubMed-9334251;

A Gum J.R. Jr., Ho J.J.L., Pratt W.S., Hicks J.W., Hill A.S.,

Gum J.R. Jr., Ho J.J.L., Pratt W.S.,

Gum J.R. Jr., Ho J.J.L., Pratt W.S.,

"MUC3 human intestinal mucin. Analysis of gene structure, the carboxyl

traminus, and a novel upstream repetitive region.";

J. Biol. Chem. 272.26678-26868 (1997).

REMBL; AF007196; AAB84383.1; -

REMBL; AF007195; AAB84383.1; -

REMBL; AF007195; BGF_11ke.

SMART; SM00181; EGF_1.

RESTIRE; PS00125; EGF_1.

RESTIRE; PS00125; EGF_1.

RESTIRE; PS01186; EGF_2: 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                 01-7NN-1998 (TrEMBLrel. 05, Created)
01-NNV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Mucin (Intestinal mucin) (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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EMBL; AF113616; AAF13032.1; -.
InterPro; IPR0000561; EGF-1ike.
InterPro; IPR000082; SEA_domain.
Pfam; PF01390; SEA; 1.
SMART; SMO0181; EGF; 2.
SMART; SMO0200; SEA; 1.
                                                                                                                                957 AA.
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PROSITE; PS01186; EGF_2; 1.
                                                                                                                                PRT;
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MEDLINE-99443732; PubMed-10512748;
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1: 1:1|||||
CLPGFSGDRC 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                       014650;
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                                                                                                                                                                       014651;
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                                                                                                                                014651
                                               RESULT 11
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                                                                                     01465
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Gaps

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                                                     Wilson R., Ainscough R., Anderson K., Baynes C.; Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lighthing J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopera A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hudson P.J.;
"Isolation of the new antigen receptor from wobbegong sharks, and use as a scaffold for the display of protein loop libraries.";
MO1. Immunol. 38:313-326(2001).
EMBL; AF336090; AAR97358.1:
InterPro: IPR003006; Ig_MHC.
InterPro: IPR00504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
New antigen receptor (Fragment).
Orectolobus maculatus (spotted wobbegong).
Enkaryota: Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
Orectolobidae; Orectolobus.
NUBL_TAXID-168098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21451048; PubMed-11566324;
Nuttall S.D., Krishnan U.V., Hattarki M., De Gori R., Irving R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 5; Length 264; Pred. No. 3.5; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                          "The sequence of C. elegans cosmid F35D2."; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                              Waterston R.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U28741; AAA68325.1; -.
HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                    165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.6%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.6
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                 Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CVIGXSGDRC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |:|||||
76 CPYGLSGDRC 85
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             Connell M.;
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Q90XX0
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DR Pfam; PF00047; 1g; 1.

DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.

KW Receptor. 165 165

SQ SEQUENCE 165 AA; 18259 MW; D4A811143C6FDE1CD CRC64;

Query Match 77.8%; Score 42; DB 13; Length 165;

Best Local Similarity 77.8%; Pred. No. 3.4;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps

Qy 2 VIGXSGDRC 10

Db 105 MIGYSGDRC 113
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Search completed: July 2, 2003, 07:28:37 Job time : 42.3333 secs

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2, 2003, 07:25:01; Search time 43.3333 Seconds (without alignments) 30.750 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                           908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                BLOSUM62DX
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                              US-09-673-785D-9
56
1 CVIGYSGDXC 10
                                                                                                                   July
                                                                                                                                                                                                Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                   Run on:
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1: SIDS2/gcdata/geneseqp-embl/AA1983.DAT: * SIDS2/gcdata/geneseqp-embl/AA1984.DAT: * SIDS2/gcdata/geneseqp-embl/AA1984.DAT: * SIDS2/gcdata/geneseqp-embl/AA1985.DAT: * SIDS2/gcdata/geneseqp-embl/AA1985.DAT: * SIDS2/gcdata/geneseqp-embl/AA1987.DAT: * SIDS2/gcdata/geneseqp-embl/AA1989.DAT: * SIDS2/gcdata/geneseqp-embl/AA1989.DAT: * SIDS2/gcdata/geneseqp-embl/AA1989.DAT: * SIDS2/gcdata/geneseqp-embl/AA1999.DAT: * SIDS2/gcdata/geneseqp-embl/AA1991.DAT: * SIDS2/gcdata/geneseqp-embl/AA1991.DAT: * SIDS2/gcdata/geneseqp-embl/AA1992.DAT: * SIDS2/gcdata/geneseqp-embl/AA1992.DAT: * SIDS2/gcdata/geneseqp-embl/AA1993.DAT: * SIDS2/gcdata/geneseqp-embl/AA1993.DAT: * SIDS2/gcdata/geneseqp-embl/AA1994.DAT: * SIDS2/gcdata/geneseqp-embl/AA1995.DAT: * SIDS2/gcdata/geneseqp-embl/AA1999.DAT: * SIDS2/gcdata/geneseqp-embl/AA2001.DAT: * SIDS2/gcdata/geneseqp-embl/AA2002.DAT: *

/SIDS2/gcgdata/geneseq/geneseqp.embl/AA1980. /SIDS2/gcgdata/geneseq/geneseqp.embl/AA1981. /SIDS2/gcgdata/geneseq/geneseqp.embl/AA1982.

A_Geneseq_101002:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CHARACO	Query Match Length DB ID Description		47 23 AAG66047 Mouse EGF motif se						53 18 AAW34467 Chimeric epidermal		
dР	Query Match Le	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100
	Score	56	26	26	26	26	26	26	26	26	7
	Result No.		7	m	4	S	9	7	80	6	-

Epidermal growth f Human EGF. Homo s Epidermal growth f Mouse epidermal gr Modified mouse epi Epidermal growth f Recombinant human	Angiotensin conver Angiotensin conver Angiotensin conver Angiotensin conver Angiotensin conver Angiotensin conver Mouse epidermal gr	Drosophila melanog Human versican iso Human cancer assoc Versican. Homo sa Chimeric epidermal Mouse NRG-2 EGF-11 N terminal of rat Rat epidermal gro	epiderani grow nan Neuregulin- L cerebellum de F fragment. Sy rget peptide fr rget peptide fr rget peptide fr	Epidermal Growth F Human EGF motif se Nicked EGF1-48. H EGF-like domain of Epidermal growth f
19 AAW50140 22 AAB37612 23 AAR175714 23 AAV76704 23 AAV76706 7 AAP60791 9 AAW68455	AAU0293 AAU0293 AAU0293 AAU0295 AAU0295	02382132	23 AAU11636 23 AAU11636 13 AAR21704 13 AAR21704 18 AAW11620 18 AAW11621	22 AAB9851 22 AAG66048 14 AAR44820 21 AAB36715 10 AAP90465
53 53 54 54 117	376 444 576 576 1073	2146 6555 2409 14 46 48 48	298 754 17 222	24444 21-880
1000.0 1000.0 1000.0 1000.0 1000.0		87.5 87.5 83.9 82.1 82.1 82.1	88888888888888888888888888888888888888	8888 88088 4.4.4.4.4.
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111 121 132 14 17	22 23 23 24	25 20 20 30 31 31 32) W W W W W W 4 -	4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

RESULT 1

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Epidermal growth factor; EGF; laminin receptor; angiogenesis; medicament; wound healing; retinopathy of immaturity; metastatic cancer; candida infection; leishmania; trichomonas vaginalis.
                                                               Mouse EGF derived peptide for targetting laminin receptor.
                                                                                                                                                                                                                                                                                                                               Nelson J, Walker B, McFerran N, Harriott P;
                                                                                                                                                                         /note= "Acetyl-Cys (S-ACM)"
10
                                                                                                                                                                                                /note= "Cys (S-Acm)-NH2"
                                                                                                                                                    Location/Qualifiers
AAY52143 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                    98GB-0008407.
                                                                                                                                                                                                                                                                                                        (UYBE-) UNIV QUEENS BELFAST
                                          28-JAN-2000 (first entry)
                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                              21-APR-1999;
                                                                                                                                                                                                                                                                                    22-APR-1998;
                                                                                                                                                                                                                     WO9954356-A1
                                                                                                                                                                                                                                          28-OCT-1999.
                    AAY52143;
                                                                                                                                Mus sp.
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Matches
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           $$$$$$$$$$$$$$$$$$$$$$$$$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                              This is a peptide derived from mouse epidermal growth factor (EGF) residues 33-42. This peptide is used in the invention to prepare a composition to target laminin receptors. EGF derived peptides inhibit blood vessel formation through their antagonism of the high affinity 67kD laminin receptor found on endothelial cells. The peptide is modified from the natural sequence to prevent protease attack. The peptide is used in the preparation of a medicament for binding to laminin receptors as an wounds and treating anglogenic diseases, especially retinopathy of immaturity. Other diseases treated include metastatic cancer, candida spp. infection, and parasitic infestations like leishmania and trichomonas vaginalis. The peptide are anti-anglogenic in human models. The peptides also inhibit both laminin and EGF-stimulated anglogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel ErbB-4 ligand, neuregulin-4 (NRG-4). NRG-4 binds to mammalian ErbB-4 receptor and can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising NRG-4 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel ErbB-4 ligand, referred as neuregulin (NRG)-4 and polynucleotide sequences encoding NRG-4, useful for upregulating or downregulating ErbB-4 receptor activity to treat Alzheimer's disease, stroke, gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ErbB-4; neuregulin-4; NRG-4; pro-NRG-4; neuroprotective; vulnerary;
cerebroprotective; vasotropic; antiparkinsonian; anticonvulsant;
cytostatic; nootropic; EGF; NRG-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                New peptide derived from murine epidermal growth factor (mEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 56; DB 21; Length 10; Pred. No. 0.064; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          and prevent tumour cell attachment to basement membranes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1c; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG66047 standard; peptide; 47 AA.
                                                                                                         Claim 4; Page 28; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
90.0%; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000US-0553769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-2001; 2001WO-IL00371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse EGF motif sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CVIGYSGDXC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-013229/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harari D, Yarden Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-041398/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200181540-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG66047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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A NAME OF A NAME
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useful for regulating an endogenous protein affecting ErbB-4 receptor activity in vivo. They are also useful for treating or preventing a disease condition or syndrome associated with disregulation of an endogenous protein affecting ErbB-4 receptor activity, e., amyotrophic endogenous protein affecting ErbB-4 receptor activity, e., amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, spinal muscular atroph trauma, stroke, ischemia, Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, neuropathy, muscular dystrophy, extramammary concer, cervical carcinoma, endometrial adenocarcinoma, pancreatic D cells-somatostatinoma and Zollinger-Eblison syndrome. The agent comprised in the pharmaceutical composition includes a polypeptide (e.g., a soluble light pharmaceutical composition includes a polypeptide (e.g., a soluble light pharmaceutical can annibody or an immunoreactive derivative of an entibody capable of binding the endogenous protein affecting ErbB-4 creceptor activity. Traceable synthetic/recombinant NRG-4-tagged molecules can serve as a diagnostic tool in which cells binding NRG-4 can be concerned sequences AAGG6604-53 represent the EGF-like motifs of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthesis of epidermal growth factor polypeptide - by condensation of protected smaller peptide sequences, de:protection then oxidn. to cyclise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The amino acid sequence is that of an epidermal growth factor tripentacontapeptide which is synthesised by condensation of protected smaller peptide sequences. This method produces the peptide smoothly, with high purity and yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56; DB 23; Length 47;
Pred. No. 0.25;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epidermal growth factor tripentacontapeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
6..20
14..31
33..42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP40315 standard; protein; 53 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11111111:1
33 CVIGYSGDRC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CVIGYSGDXC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP59027858-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-1984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP40315;
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epithelial wounds; gastric acid secrection.
                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                       89US-0351773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88US-0284533.
                                                                                      90WO-0S02600
                                                                                                                                                                                                                                                                                                            90.06;
                                                                                                                                                                                                                                                                                                                                                                                                 AAR67275 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88US-0284533
                             11..11
/label= E,
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic human/mouse EGF
                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 90.C
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                               1 CVIGYSGDXC 10
                                                                                                                                                           WPI; 1990-361427/48.
                                                                                                                        (CHIR-) CHIRON CORP
                                                                                                                                                                                                                                                                 See also AAR08004
                                                                                                                                                                                                                                                                                  53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                         Nascimento CG,
                                                                                      09-MAY-1990;
                                                                                                      12-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1995
                                                    WO9013570-A.
                                                                     15-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAR67275;
                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                      The inventors claim synthetic peptides which correspond to sequences occurring in EGF, but excluding EGF. The synthetic peptides correspond to active sequences from EGF fragments: 3·14, 12·14, 12·15, 3·10, 29·37 and 33·37 (Claims 2·7 and AAP91659-p91664 resp.). The peptides are anglogenic. Their relative shortness means that they pose fewer synthesis problems than the entire EGF molecule.
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                  Amino acid sequence for naturally occurring epidermal growth factor
                                                                                                                                                                                                                                                                                                                                   Synthetic peptide active in stimulating angiogenesis - has sequences corresponding to amino acid sequences occuring in epidermal growth factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified murine epidermal growth factor; stability; storage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 53;
                  5; Length 53;
                                  Indels
                                                                                                                                                                                            Epidermal growth factor; angiogenesis; synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 10;
Pred. No. 0.28;
Mismatches 0;
                 , DB 5
0.28;
                Score 56; DB
Pred. No. 0.28
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified murine epidermal growth factor.
                                                                                                              AAP91658 standard; protein; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR08007 standard; protein; 53 AA.
                                                                                                                                                                                                                                                                                (CSIR ) COMMONWEALTH SCIENT ORG.
                 100.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
                                                                                                                                                                                                                                               88WO-AU00300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.06;
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Fig 1; 1/1; 11pp; English.
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                   10
                                                            1 CVIGYSGDXC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
9, Conserve
                                                                                                                                                                                                                                                                                                                  WPI; 1989-068852/09.
                                                  1 CVIGYSGDXC
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 AA;
Ŗ,
53
                                                                                                                                                                                                                                               10-AUG-1988;
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                                                                                                                                                                                                                                                                                                  McAuslan BR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1991
                                                                                                                                                29-JUN-1990
                                                                                                                                                                                                            WO8901489-A
                                                                                                                                                                                                                              23-FEB-1989
Sequence
                                                                                                                                AAP91658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR08007;
                                                                                                                                                                           (EGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
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ID AAR
                                                                                              RESULT
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Cell growth factor; viscoelastic solution; fibroblastic growth factor; FGF; epidermal growth factor; EGF; buffered solution; lubrication; carboxypropyl methylcellulose; cellulose gum; dextran; dextran sulphate; chondroitin sulphate; sodium hyaluronate; osmolarity; mitogenic; wound healing; cell protection; cell coating; surgery; tissue space; hydroxypropyl methylcellulose; manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The human rEGF is used to treat oversecretion of gastric acid or epithelial wound. EGF is modified to increase its chemical stability. Its storage life is improved without diminishing its biological activity. The proteins may be prepared by traditional chemical or recombinant means.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human epidermal growth factor - is substituted at position 11 greater stability and improved storage life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 11; Length 53;
red. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Given in the specification as Try"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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1; Mismatches
...r
Misc-difference 11..11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                  0, A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 25; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medina-Selby A;
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chimeric EGF protein contains sequences derived from human and mouse EGF sequences. The chimeric EGF proteins can be recombinantly produced by culturing a microorganism of the genus Bacillus transformed by an expression vector containing the encoding DNA molecules. The recombinant chimeric EGF proteins exhibit a wide variety of physiological activities similar to those of naturally occurring EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Epidermal growth factor; EGF; chimeric; human; mouse; recombinant.
                                                                                                                                                       Chimeric epidermal growth factor proteins - and DNA molecules for
                                                                                                                                                                                                                                           This is a chimeric epidermal growth factor (EGF) protein AC. This
                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 18; Length 53; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "region C from mouse EGF"
48..53
/note= "region D from human EGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric epidermal growth factor protein ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "region A from mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "region C from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "region B from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW34467 standard; Protein; 53 AA.
                                                                                                                                                                                                          Claim 5; Page 26; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
90.0%; P
                                                                                                                                                                      their recombinant production
     96JP-0123970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Mus sp.
- Homo sapiens.
                                      (HGET ) HIGETA SHOYU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HGET ) HIGETA SHOYU KK
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/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 CVIGYSGDRC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CVIGYSGDXC 10
                                                                                                                                                                                                                                                                                                                                                                                           Fagami H, Tanaka A;
                                                                                                    WPI; 1997-550187/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ragami H, Tanaka A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-550187/51.
                                                                                                                                                                                                                                                                                                                                                                             53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT99942
                                                                                                                       N-PSDB; AAT99941
 23-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU9717759-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Region
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     g
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                                                                                                                                                                                                                                                  The sequences given in AAR67273-76 are cell growth factors which may be used in the viscoelastic solution of the invention. The peptides growth factor (FGF) and epidermal growth factor (FGF) and epidermal growth factor (FGF). The viscoelastic solution also comprises a buffered solution which is pref. a buffered balanced salt solution, at least 1 of hydroxy or carboxypropyl methylcellulose, actilulose gum, dextran or dextran sulphate, chondroitin sulphate, and sodium hyaluronate. It has a pH of 6-8 and an osmolarity of 200-400 moSmol/1. The growth factors are mitogenic in vitro for a wide range of tissues and the viscoelastic soln. May be used as a surgical soln. which is in direct contact with cells undergoing wound healing. It also provides a cell protection and cell coating during surgery. The soln. provides maintenance of tissue space, hydroxypropyl methylcellulose and chondroitin sulphate lubricate the tissue, while sodium hyaluronate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Epidermal growth factor; EGF; chimeric; human; mouse; recombinant.
                                                                                                                                                   Viscoelastic soln. contg. hydroxypropyl methylcellulose, sodium hyaluronate, chondroitin sulphate and growth factors - used as surgical soln. to promote wound healing, e.g. of corneal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 16; Length 53;
Pred. No. 0.28;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "region B from human EGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric epidermal growth factor protein AC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "region C from mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "region D from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                        Disclosure; Column 5; 8pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW34466 standard; Protein; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               provides tissue manipulation
 89US-0434305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 90.C
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Homo sapiens.
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/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                    Skelnik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CVIGYSGDXC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LIND/) LINDSTROM R L.
                                                                                                                   WPI; 1995-005865/01
                                                    (SKEL/) SKELNIK D.
                                                                                  Lindstrom RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Mus
Chimeric - Homo
13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-APR-1997;
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AAW34466

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Gaps

Gaps

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ö DB 19;

Length 53; Indels

Score 56; DB 1.

100.0%;

Pred. No. 0.28 1; Mismatches

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centrifugation or membrane filtration.
                                                                                 Conservative
                                                                                                           1 CVIGYSGDXC 10
                                                                                                                            33 CVIGYSGDRC 42
                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53. AA;
                             53 AA;
                                                                                                                                                                                                                                                                                                                                                       Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolation of
                                                                                                                                                                                                                                                            08-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                 AU9728698-A.
                                                                              9;
                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyauchi A,
                               Seguence
                                                                                                                                                                                                                                  AAW50139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                             RESULT 10
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                                                                                 Matches
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                                                                                                                                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents mouse epidermal growth factor (BGF)

from the present invention. The present invention describes a method for
the isolation of recombinant epidermal growth factor (EGF) from whole
broth. The method comprises: (a) passing a culture containing the
choth. The method comprises: (a) passing a culture containing the
protein upwards through a column containing a fluidised bed of ion
cachanger, washing the ion exchanger to remove non-adsorbed material,
allowing the ion exchanger to settle, and eluting adsorbed protein by
passing an eluant downwards through the column; (b) filtering the eluate
through a membrane with a molecular weight cutoff of 10000, and (c)
concentrating the filtrate on a membrane with a molecular weight cutoff
of 5000. The method is for isolating recombinant human, mouse, pig or
cat EGF, or an EGF analogue with one of four defined amino acid sequences
(given in the specification), from Bacillus brevis cultures. The EGF
proteins can be recovered in high yield and high purity without the need
to pretreat the culture broth to remove the cells, e.g. by costly
                                                                                                                                                                                                                                  ö
                                                                This is a chimeric epidermal growth factor (EGF) protein ABC. This chimeric EGF protein contains sequences derived from human and mouse EGF sequences. The chimeric EGF proteins can be recombinantly produced by culturing a microorganism of the genus Bacillus transformed by an expression vector containing the encoding DNA molecules. The recombinant chimeric EGF proteins exhibit a wide variety of physiological activities similar to those of naturally occurring EGF.
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolation of recombinant epidermal growth factor from whole broth
Chimeric epidermal growth factor proteins - and DNA molecules for
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolation; recombinant;
                                                                                                                                                                                                     Score 56; DB 18; Length 53;
Pred. No. 0.28;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; epidermal growth factor; EGF; isolation to exchange chromatography; Bacillus brevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by fluidised-bed ion-exchange chromatography
                                                                                                                                                                                                                                                                                                                                                      AAW50134 standard; protein; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Warren B;
                                       Claim 6; Page 26; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 26; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse epidermal growth factor.
                                                                                                                                                                                                      100.0%;
               their recombinant production
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                                                                                                                                                                                                                   90.06;
                                                                                                                                                                                                                                                                                                                                                                                                         08-JUL-1998 (first entry)
                                                                                                                                                                                       Query Match
Best Local Similarity 90.0.
Pest Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miyauchi A, Nemoto A,
                                                                                                                                                                                                                                                          1 CVIGYSGDXC 10
                                                                                                                                                                                                                                                                        CVIGYSGDRC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-131057/13
                                                                                                                                                                           53 AA;
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                                                                                                                                                                                                                                                                                                                                                                               AAW50134;
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus sp.
                                                                                                                                                                                                                                                                                                                                         AAW50134
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factor (EGF) like activity, from the present invention. The present actor (EGF) like activity, from the present invention describes a method for the isolation of recombinant epidermal growth factor (EGF) from whole broth. The method comprises: (a) passing a culture containing the protein upwards through a column containing a fluidised bed of ion exchanger, washing the ion exchanger to remove non-adsorbed protein by passing an eluant downwards through the column; (b) calsorbed protein by passing an eluant downwards through the column; (b) filtering the eluate through a membrane with a molecular weight cutoff of 10000, and (c) concentrating the filtrate on a membrane with a molecular weight cutoff of 5000. The method is for isolating recombinant human, mouse, pig or rat EGF, or an EGF analogue with one of four chuman, mouse, pig or rat EGF, or an EGF analogue with one of four chuman, mouse, pig or tat EGF, or an EGF analogue with one of four chuman, mouse, pig or tat EGF, or an EGF analogue with one of four chuman, mouse, pig or tat EGF, or an EGF analogue with one of four chuman, mouse, pig or tat EGF, or an EGF analogue with one of four chuman, mouse, pig or tat EGF, or an EGF analogue with one of four chuman, mouse, pig or tat EGF, or an EGF analogue with one protein or analogue with one of four contents cultures. The EGF proteins can be recovered in high yield and high purity without the need to pretreat the culture broth to remove the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a protein which has epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant epidermal growth factor from whole broth -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 0.28;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                     Epidermal growth factor; EGF; isolation; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                    ion exchange chromatography; Bacillus brevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by fluidised-bed ion-exchange chromatography
                                                                                                                                                                                                                                                                          Epidermal growth factor analogue 3
AAW50139 standard; protein; 53 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
90.0%; 1
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                                                                                                                                                                                         (first entry)
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hes 9; Conserv
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AAW50140;

RESULT 11

AAW50140

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fragment of a Plasmodium mercocite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of plasmodium MSP-1_4_2. compared to natural MSP-1_1_9. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is human epidezmal growth factor (EGF). This sequence was used in a sequence homology comparison with the wild-type MSP-1 protein from P. falciparum (see AAB37608), which was used to generate the variants of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised form; monoclonal antibody alpha 340; gene therapy;
epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast;
gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Epidermal growth factor (EGF) used in exemplification of the invention.
                Merozoite surface protein; protazoacide; vaccine; malaria; human; EGF;
                                                                                                                                                                                                                                                                                                                                                               Uthaipibull C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to non-natural variants of a C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 22; Length 53; Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                               Morgan W,
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                          Holder A, Birdsall B, Feeney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE15714 standard; Protein; 53 AA.
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99US-0311817.
                                                                                                                                                                                                                                                                                                                       (MEDI-) MEDICAL RES COUNCIL.
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                                                                                                                                                                                               20-APR-2000; 2000WO-GB01558
                                                                                                                                                                                                                                                                               99CA-2271451
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Matches 9; Conservative
                                   epidermal growth factor.
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                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-015762/02.
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                                                                                                               WO200063245-A2
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                                                                                                                                                                                                                                     20-APR-1999;
13-MAY-1999;
25-MAY-1999;
                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                         26-OCT-2000
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AAE15714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a protein which has epidermal growth factor (BGF) like activity, from the present invention. The present invention describes a method for the isolation of recombinant epidermal growth factor (BGF) from whole broth. The method comprises: (a) passing a culture containing the protein upwards through a column containing a fluidised bed of ion exchanger, washing the ion exchanger to remove non-adsorbed protein by passing an eluant downwards through the column; (b) filtering the eluate through a membrane with a molecular weight cutoff of 10000, and (c) concentrating the filtrate on a membrane with a molecular weight cutoff of 5000. The method is for isolating recombinant human, mouse, pig or rat EGF, or an EGF analogue with one of four defined amino acid sequences (given in the specification), from Bacillus breath with whithout the need to pretreat the culture broth to remove the cells, e.g. by costly centrifugation or membrane filtration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 56; DB 19; Length 53;
Pred. No. 0.28;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                   Epidermal growth factor; EGF; isolation; recombinant; ion exchange chromatography; Bacillus brevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by fluidised-bed ion-exchange chromatography
                                                                                                                                                                                               Epidermal growth factor analogue 4.
                                                                     AAW50140 standard; protein; 53 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Warren B;
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90.0%; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nemoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
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es 9; Conserv
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                                                                                                                                                                                                                                                                                             Unidentified
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                                                                                                                                                                                                                                                                                                                                                                             05-FEB-1998
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Gaps

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Human EGF.

AAB37612;

DEXTACK

RESULT 12

AAB37612

Sequence

Query Match

Matches

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polynucleotides (1). The method comprises contacting a population of single-stranded scaffold fragments (SF) with population of donor fragments (BF) to form a complex (II) comprising at least one SF whybridised to two DFs. (II) is treated so that single stranded regions of (II) are filled-in and adjacent fragments are ligated. (MI) is useful for a directed evolution process which involves forming a library of (I) that can be screened for a characteristic of interest. Subsequent rounds of directed evolution can produce chimeric polynucleotides with an improved characteristic of interest. The methods facilitate the concerning of chimeric polynucleotides with an improved characteristic polynucleotides and do not require hybridising concerning process does not rely upon a contiguous, full-length cemplate, it is unnecessary to modify a template to facilitate its removal. This is the amino acid sequence of the mouse epidermal growth factor (EGF) used to demonstrate a method of in vitro recombination
                                                                                                                                                                                                                                                                                                                                               Forming chimeric polynucleotide by contacting single-stranded (ss) scaffold fragment, and donor fragment populations to form hybridised complex having ss regions which are filled-in, and ligating adjacent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; epidermal growth factor; receptor; EGF; chimeric polynucleotide; directed evolution; chimeragenesis; recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a method of forming (MI) chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified mouse epidermal growth factor (EGF).
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                                                                                                                                                                                                                          Coco WM, Encell LP, Arensdorf JJ;
                                                                                                                                                                         (ENCH-) ENCHIRA BIOTECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU76706 standard; Protein; 54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 3; 65pp; English.
18-JUL-2001; 2001WO-US22640.
                                              18-JUL-2000; 2000US-218921P.
18-JUL-2000; 2000US-2190B5P.
18-OCT-2000; 2000US-0691B73.
19-OCT-2000; 2000US-0692732.
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Best Local Similarity 90.0
---- 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 AA;
                                                                                                                                                                                                                                                                                                N-PSDB; ABK10313.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation schedules. The humanised form of the antibody 340 has reduced immunospenicity but shows similar binding to cells expressing EGF receptor, as the original murine antibody and has increased ability to inhibit the growth of EGF receptor expressing cells. The invention is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                         New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 23; Length 53;
Pred. No. 0.28;
1; Mismatches 0; Indels
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/note- "Encoded by TAA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU76704 standard; Protein; 54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Fig 12; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
                    21-MAY-2001; 2001WO-GB02226.
                                                                   19-MAY-2000; 2000GB-0011981.
24-AUG-2000; 2000GB-0020794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.08;
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                   Durrant LG;
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                                                                                                                                                 (SCAN-) SCANCELL LID.
                                                                                                                                                                                                                                               WPI; 2002-062384/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 AA;
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Misc-difference
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                                                                                                                                                                                                Ellis JRM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU76704;
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NAME OF THE PROPERTY OF THE PR
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Gaps

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; Score 56; DB 23; Length 54; Pred. No. 0.28; 1; Mismatches 0; Indels

100.0%;

90.06;

24-JAN-2002.

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The invention uscentibut of toliming (m.) channeric polynucleotides (I). The method comprises contacting a population of single-stranded scaffold fragments (SF) with population of donor fragments (BF) to form a complex (II) comprising at least one SF hybridised to two DFs. (II) is treated so that single stranded regions of (II) are filled-in and adjacent fragments are ligated. (M.) is useful for a directed evolution process which involves forming a library of (I) that can be screened for a characteristic of interest. Subsequent rounds of directed evolution can produce chimeric polynucleotides with an improved characteristic of interest. The methods facilitate the generation of chimeric polynucleotides and do not require hybridising donor fragments to a target- or full-length template. Because the chimeric chimeric polynucleotides and contiguous, full-length chimeragenesis process does not rely upon a contiguous, full-length chimeragenesis process does not rely upon a contiguous, full-length chimeragenesis the amino acid sequence of a mouse epidermal growth factor (EGF) modified to make it as similar as possible to the human protein (AAU76705) and used to demonstrate a method of in vitro
                                                                                                                                                                                                                                                                                                                                                Forming chimeric polynucleotide by contacting single-stranded (ss) scaffold fragment, and donor fragment populations to form hybridised complex having ss regions which are filled-in, and ligating adjacent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a method of forming (M1) chimeric
                                                                                                                                                                                                (ENCH-) ENCHIRA BIOTECHNOLOGY CORP.
                                                                                                                                                                                                                                           Encell LP, Arensdorf JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 3; 65pp; English.
                                                                                  18-JUL-2000; 2000US-218921P.
18-JUL-2000; 2000US-219085P.
19-CCT-2000; 2000US-0691873.
19-CCT-2000; 2000US-0692732.
                                           18-JUL-2001; 2001WO-US22640.
                                                                                                                                                                                                                                                                                     WPI; 2002-179795/23.
N-PSDB; ABK10315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     fragments
                                                                                                                                                                                                                                         Coco WM,
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Ouery Match

Ouery Match

Best Local Similarity 90.0%; Pred. No. 0.2%;

Matches 9; Conservative 1; Mismatches 0; Indels 33 CVIGYSGDRC 42 1 CVIGYSGDXC 10 ò

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Gaps

; 0

2, 2003, 07:30:55 Search completed: July Job time: 44.3333 secs

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Sequence 2, Appli
Patent No. 5183805
Patent No. 5183805
Patent No. 528643
Sequence 14, Appl
Sequence 14, Appl
Sequence 24, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Patent No. 5332669
Patent No. 5180808
Sequence 10, Appl
Sequence 10, Appl
Patent No. 5332669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                    July 2, 2003, 07:25:01; Search time 10.6667 Seconds (without alignments) 27.584 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-457-135-7
US-08-284-923-2
US-08-619-032B-2
5332669-2
5180808-2
US-09-191-647-10
US-09-540-153-10
5332669-1
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US-09-158-710-14

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US-08-278-089A-24

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US-09-126-121-12

US-08-753-007A-17
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US-09-101-544-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                                                                        OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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56
1 CVIGYSGDXC 10
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
No.
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Sequence 15, Appl Patent No. 5434135 Patent No. 5177197

5177197-50

Sequence 13, Sequence 15,

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            Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Patent No. 5332669
Patent No. 5344135
Patent No. 5248093
Sequence 13, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 13, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTOTE: BW PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/597,545
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                      Delta-Like Gene Expressed In
Neuroendocrine Tumors
                                                US-08-619-032B-1
5434135-2
5434135-2
54369-3
54369-3
5218093-1
US-07-845-089B-13
US-08-456-201-15
US-08-456-241-15
US-08-440-401-13
US-08-419-878B-13
US-08-419-878B-13
US-08-419-878B-13
                                                                                                                                                                                                               PCT-US92-04295A-15
US-08-343-401A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,537
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 40399/166 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08597545

Patent No. 5580738

GRERAL INFORMATION:

TITLE OF INVENTION: Delta-Like Gene Expres

CORRESPONDENCE ADDRESS:

ADDRESSE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA
                          US-08-360-841-2
US-08-861-000-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
90.0%; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-597-545-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
US-08-597-545-7
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GENERAL INFORMATION:
APPLICANT: Blancy, Jeffrcy M.
APPLICANT: Blancy, Jeffrcy M.
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: MUTELNS OF EPIDERMAL GROWTH FACTOR
TITLE OF INVENTION: EXHIBITING ENHANCED BINDING AT LOW PH
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: Intellectual Property R-440, P.O. Box 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 1; Length 53; red. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 9466-8097

COUNTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,032B
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Guth, Joseph H.
REGISTRATION NUMBER: 31,261
REFERENCE/DOCKET NUMBER: 31,261
REFERENCE/DOCKET NUMBER: 0231.004
TELEPRAK: (510) 923-3888
TELEFRAK: (510) 655-3542
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                            FILING DATE:
CLASSIFICATION: 435
PLOR APPLICATION DATA:
APPLICATION NUMBER: US 07/746,651
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,923
                                                                                                                                                                                                           NAME: McClung, Barbara G
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 231.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
TELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08619032B Patent No. 6191106
                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 53 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative 1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-284-923-2
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STATE:
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| Sequence 2, Application US/08284923
| Sequence 2, Application US/08284923
| Patent No. 5547935
| GENERAL INFORMATION:
| APPLICANT: Mullenbach, Guy T
| APPLICANT: Blaney, Jeffrey M
| APPLICANT: Rosenberg, Steven
| TITLE OF INVENTION: muteins of Epidermal Growth Factor
| TITLE OF INVENTION: exhibiting enhanced binding at low ph
| NUMBER OF SEQUENCE: 2
| CORRESPONDERS: 2
| CORRESPONDERS: 2
| CORRESPONDERS: 3
| CITY: Emeryville
| CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 56; DB 1; Length 12;
Pred. No. 0.011;
1; Mismatches 0; Indels
                                                  Sequence 7, Application US/08457135
Fatent No. 5644031
GENERAL INFORMATION:
APPLICANT: LABORDA, Jorge
TITLE OF INVENTION: Delta-Like Gene Expressed In TITLE OF INVENTION: Neuroendocrine Tumors
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                          COUNTRY WASAILINGTON, D.C.
COUNTRY: USA

2 IP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PG-BOS/MS-DOS
SOFTWARE: PATENTIN PG-BOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/457,135
FILING DATE: 01-JUN-1995
FILING DATE: 11-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAMM: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30,399/304/NIHD
TELECOMMUNICATION INFORMATION:
may FORMATION INFORMATION:
may FORMATION INFORMATION:
may FORMATION INFORMATION:
may FORMATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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90.0%; E
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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(202)672-5399
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Best Local Similarity 90.07
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                                    us-08-457-135-7
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Fatent No. 6270984
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Rid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
FILE REPERENCE: 1998-031-3
CURRENT APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1999-11-14
FRIOR APPLICATION NUMBER: 60/065,544
FRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                              Length 154;
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APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
                                                                                                                                                                                              Score 48; DB 3;
Pred. No. 1.9;
4; Mismatches (
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Pred. No. 1.9;
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CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/191,647
PRIOR FILING DATE: 1998-11-13
PRIOR PLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
                    60/081,057
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EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: 60/08.
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 10
LENGTH: 154
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60.0%;
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60.0%;
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 60.0
Local 6, Conservative
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Best Local Similarity 60.0.
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11 CMLGYTGDNC 20
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                                                                                                                          ; TYPE: PRT
; ORGANISM: mouse
US-09-191-647-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: mouse
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LENGTH: 154
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TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN
ANTIBOLIES, AND METHODS OF DETECTING THE SAME
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 6; Length 2409;
Pred. No. 19;
                                                                      ; Score 56; DB 4; Length 53; Pred. No. 0.045; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB 6; Length 53; Pred. No. 0.045; 1; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
ITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
                                                                                                                                                                                                                                                                 Patent No. 5332669

APPLICANT: DEUEL, THOMAS F.

TILE OF INVENTION: PROSTATE-DERIVED MITOGEN

NUMBER OF SEQUENCES: 3

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/356,739

FILING DATE: 24 MAR-1989
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APPLICATION NUMBER: US/07/441,179
FILING DATE: 27-NOV-1989
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EARLIER APPLICATION NUMBER: 60/065,544
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Patent No. 6046015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
90.0%;
                                                                    Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative 1
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80.0%;
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Best Local Similarity 80.0°
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Best Local Similarity 90.0
Matches 9; Conservative
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-619-0328-2
                                                                                                                                                               33 CVIGYSGDRC 42
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                                                                                                                                          1 CVIGYSGDXC 10
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                                                                          Length 754;
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                                                                                                     1; Indels
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                                                                                                                                                                                                                         Patent No. 5183805
Patent No. 5183805
TILE ON INVENTION: BIOACTIVE EGF PEPTIDES FOR PROMOTION OF TISSUE REGENERATION AND CANCER THERAPY
CURRENT APPLICATION DATE: 13-AUG-1990
FILING DATE: 13-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
5183805-2
7 PATENT NO. 5183805
7 PATENT LEE, JIN S., BLICK, MARK
TITLE OF INVENTION: BIOACTIVE EGF PEPTIDES FOR
PROMOTION OF TISSUE RECENERATION AND CANCER THERAPY
                                                                       Score 46; DB 2;
Pred. No. 18;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
5256643-8
; Patent No. 5256643
; TITLE OF INVENTION: HUMAN CRIPTO PROFEIN
; VUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/567,407
FILING DATE: 13-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/530,165
FILING DATE: 29-MAY-1990
                                                                       82.1%;
60.0%;
                                                                                Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0°
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-864A-2
                                                                                                                                              1 :||:||:|
280 CPVGYTGDRC 289
                                                                                                                             1 CVIGYSGDXC 10
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5183805-1
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5256643-8
                                                                       Query Match
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                                                                                       Score 48; DB 4;
Pred. No. 1.9;
                                                                                                                                                                                                                                           ent No. 5332669
APPLICANT: DEDEL, THOMAS F.
TILLE OF INVENTION: PROSTATE-DERIVED MITOGEN
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
FILLING DATE: 24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB (Pred. No. 1.3; 2; Mismatches
                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,864A
FILING DATE: 8-5EP-1995
CLASSIFFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KAIA, CATHERING J.
REGISTRATION NUMBER: 41.106
REFERENCE/DOCKET NUMBER: 41.106
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                       85.7%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 82.1%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 754 amino acids
                                                                       Ouery Match
Best Local Similarity 60.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 754 amino acids
amino acid
                                                                                                                                              1 CVIGYSGDXC 10
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|11 CMLGYTGDNC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CVIGYSGDXC 10
                                          ; ORGANISM: mouse US-09-540-153-10
                                                                                                                                                                                                                                                                                                                                                              LENGIH: 48
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SEQ ID NO 10
LENGTH: 154
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                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:1
                                                                                                                                                                                                                                              ; Patent No.
                                                                                                                                                                                                                   RESULT 10
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us-09-673-785d-9.jull.rai

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                       0; Gaps
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                                                                                                                                                            RESULT 15
US-08-039-364-14
Sequence 14, Application US/08039364
Sequence 14, Application US/08039364
Sequence 14, Application US/08039364
Sequence 14, Application US/08039364
Sequence 14, Application
Sequence 14, Application
Septimental Machanal Michael
Septimental Migashiyama, Shigeki
APPLICANT: Besner, Gail F.
TITLE OF INVENTION: HEPARIN BINDING MITOGEN WITH
TITLE OF INVENTION: HOMOLOGY TO EPIDERMAL GROWTH FACTOR
TITLE OF INVENTION: HOMOLOGY TO EPIDERMAL GROWTH FACTOR
TITLE OF INVENTION: HOMOLOGY TO EPIDERMAL GROWTH FACTOR
SUMBER OF SEQUENCES: 18
SCORESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                       1; Indels
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Pred. No. 1.4;
3; Mismatches
Best Local Similarity 60.0%; Pred. No. 0.96; Matches 6; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: TBM PS.2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/039,364
FILING DATE: 15 JUN 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/598,082
FILING DATE: 16 OCT 1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENDE/DOCKET NUMBER: 05162/002002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHANGE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: July 2, 2003, 07:25:43
Job time: 11 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 37 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
1 TOPOLOGY: linear
US-08-039-364-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.4
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                1 CVIGYSGDXC 10
                                                                                          ||:|| |::|
13 CVVGYIGERC 22
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28 CVVGYIGERC 37
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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 2, 2003, 07:28:49; Search time 103 Seconds (without alignments) 11.164 Million cell updates/sec Run on:

US-09-673-785D-9 56: 1 CVIGYSGDXC 10 Perfect score:

Scoring table: Sednence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5

440863 seqs, 114992915 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.Pep:* /cgn2_6/ptodata/2/pubpaa/VGOB_PUBCOMB.Pep:* /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:* 6/ptodata/2/pubpaa/US06_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 19, Appl	Sequence 33,			S	Sequence 4,	S	-				Sequence 13, A	Sequence 9,		Sequence 4, A	1	Sequence 3,	Sequence 13,	
ID	US-10-138-158-1	US-10-150-648B-	US-10-150-648B-	US-09-925-301-	US-10-211-994-20	US-09-864-675-	US-10-136-573A-	US-09-877-665-1	US-10-215-862-1	US-09-817-647-	US-10-096-241-	US-10-201-945-13	US-09-903-327A-	US-10-150-648B-	US-10-211-994-4	US-09-848-664-31	US-09-934-706-3	US-10-022-609-13	US-10-211-994-27
DB	6	6	φ	10	6	10	6	σ	φ	10	12	Φ	6	σ	σ	10	10	6	6
å Query Match Length DB	53	53	145	741	112	298	46	46	46	46	47	48	53	53	53	53	28	91	111
& Query Match	100.0	100.0	100.0	87.5	82.1	82.1	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4
Score	26	26	26	49	46	46	45	45	45	45	45	45	45	45	45	45	45	45	45
Result No.	-	7	m	4	Ň	9	7	æ	თ	10	11	12	13	14	15	16	17	18	19

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1 CVIGYSGDXC 10 111111111:4 33 CVIGYSGDRC 42

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Sequence 29, Appl Sequence 5, Appli Sequence 7, Appli Sequence 25, Appl	6. 35.25 4 4 4 4 4	Sequence 4, Appli Sequence 7, Appli Sequence 5, Appli Sequence 4, Appli Sequence 6,533, Ap	269, 34, B 31, B 266, 273,	Sequence 7.7, App Sequence 6, Appli Sequence 8, Appli Sequence 2, Appli Sequence 171, App Sequence 342, App
9 US-10-211-994-29 9 US-10-211-994-5 9 US-10-211-994-7 9 US-10-211-994-25 10 US-09-280-53-64	9 US-10-150-648B-32 10 US-09-934-706-5 9 US-09-903-327A-13 9 US-09-903-327A-13 10 US-09-908-322-6	9 US-10-024-599-4 9 US-09-900-449A-7 9 US-09-900-449A-5 9 US-09-900-449A-4 9 US-10-106-698-6253		9 US-10-20-704-272 9 US-09-900-449A-6 9 US-09-900-449A-8 9 US-09-900-449A-2 9 US-10-157-031-171 9 US-09-759-130B-342
111111111111111111111111111111111111111	146 400 493 832 832	176 572 601 639 384	53 145 211 427	966 566 774 878 883
88888 4.4.4.4.4		~~~~	75.	75.0
44444 888	144444 10000000	4 4 4 4 4 4 4 4 4 4	44444	4 4 4 4 4 4 4 4 4 4
20 21 23 23	552 552 562 562 563 563 563 563 563 563 563 563 563 563	3 3 3 3 3 3 4 3 5 4 5 5 5 5 5 5 5 5 5 5		44444 0112645

ALIGNMENTS

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Sequence 19, Application US/10138158

Sequence 19, Application US/10138158

Sublication No. US20030036509A1

GENERAL INFORMATION:
APPLICANT: STEM CELL PHARMACEUTICALS, INC.
APPLICANT: TWARDIEK, Thomiel R.
APPLICANT: FELKER, Thomies S.
APPLICANT: FELKER, Thomies S.
TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS AND METHODS OF U.
TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS OF U.
TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS OF U.
TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS OF U.
FILE REFERENCE: STEMILIO-66.
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: US 09/459,813
PRIOR FILING DATE: 2000-01-27
PRIOR PRIOR FILING DATE: 2000-01-27
PRIOR PRIOR FILING DATE: 2000-01-27
PRIOR PRIO
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Pred. No. 0.064;
1; Mismatches 0; Indels
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90.0%; P
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Best Local Similarity 90.0

Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-138-158-19
US-10-138-158-19
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (282)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                     ; DATABASE ACCESSION NUMBER: GenBank Accession No. US20030059802A1 J00380
; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: Relevant residues FROM 919 TO 1063
US-10-150-648B-30
                                                                                                                                                                                                                          Gaps
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Fatent No. US20020052308A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05882
FRIOR APPLICATION NUMBER: E07/US00/05882
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR FILING DATE: 1999-03-12
                                                                                                                                                                 100.0%; Score 56; DB 9; Length 145; 90.0%; Pred. No. 0.15; 1. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49; DB 10; Length 741;
Pred. No. 7.2;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Rao, M.R.S.
APPLICANT: Sengupta, Paromita
APPLICANT: Burman, Anand C.
APPLICANT: Burman, Anand C.
APPLICANT: Mukharjee, Rama
APPLICANT: Thomas, Becky
ITLE OF INVENTION MULTIVALENT SYNTHETIC VACCINE FOR CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/211,994
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION WIMBER: 60/309,975
PRIOR FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/10211994 Publication No. US20030082201A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.5%;
80.0%;
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                              Query Match 100.
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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460 CVPGYSGDQC 469
                                                                                                                                                                                                                                                                       1 CVIGYSGDXC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-925-301-930
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US-10-211-994-20
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LENGTH: 741
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                                                                                                                                   APPLICANT: John, Sushil J.
APPLICANT: John, Sushil J.
APPLICANT: Selinger, Leonard B.
APPLICANT: Selinger, Leonard B.
APPLICANT: Benkel, Bernhard F.
TITLE OF INVENTION: Nacleic acid and protein sequences of bovine epidermal growth FILE OF INVENTION: factor
FILE REPERENCE: 60-01
CURRENT APPLICATION NUMBER: US/10/150,648B
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/292,136
PRIOR FILING DATE: 2001-05-18
SOFTWARE: Patentin version 3.1
SEQ ID NO 33
LENGTH: 53
LENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: John, Sushil J.
APPLICANT: Schinger, Leonard B.
APPLICANT: Schinger, Leonard B.
APPLICANT: Schinger, Leonard B.
APPLICANT: Benkel, Bernhard F.
TITLE OF INVENTION: Nucleic acid and protein sequences of bovine epidermal growth
TITLE OF INVENTION: factor
TITLE OF INVENTION: factor
TITLE OF INVENTION: factor
CURRENT APPLICATION NUMBER: US/10/150,648B
CURRENT FILING DATE: 2002-05-17
PRIOR PFLICATION NUMBER: 60/292,136
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
LENGTH: 145
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TITLE: Nucleotide sequence of epidermal growth factor cDNA predicts a

TITLE: 128,000-molecular weight protein precursor
JOURNAL: Nature

VOLUME: 303
PAGES: 722-725
PAGES: 722-725
DATABASE ACCESSION NUMBER: GenBank Accession No. US20030059802AI J00380
PATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: Relevant residues FROM 977 TO 1029
US-10-150-648B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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TITLE: Nucleotide sequence of epidermal growth factor cDNA predicts a
TITLE: 128,000-molecular weight protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30, Application US/10150648B Publication No. US20030059802Al GENERAL INFORMATION:
APPLICANT: Bilodeau-Goesseels, Sylvie
                                                                                                                         APPLICANT: Bilodeau-Goesseels, Sylvie
APPLICANT: John, Sushil J.
                                                   Sequence 33, Application US/10150648B Publication No. US20030059802A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CVIGYSGDXC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus PUBLICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL: Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VOLUME: 303
PAGES: 722-725
RESULT 2
US-10-150-648B-33
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US-10-150-648B-30
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DB 9; Length 46;

Score 45;

us-09-673-785d-9.jull.rapb

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80.48;
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                                                                               Conservative
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                                                                                                                       1 CVIGYSGDXC 10
                                                                                                                                               32 CVVGYIGERC 41
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32 CVVGYIGERC 41
                                       Query Match
Best Local Similarity
Matches 6; Conserva
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Best Local Similarity
Matches 6; Conserve
  US-10-136-573A-12
                                                                                                                                                                                                                                             US-09-877-665-12
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                                                                                                                                                                                                                            RESULT 8
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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie Rose
APPLICANT: Abang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and
TITLE OF INVENTION: Uses Therefor
TITLE OF INVENTION: Uses Therefor
TITLE OF INVENTION: Uses Therefor
CURRENT APPLICATION NUMBER: US, 10, 136, 573A
CURRENT FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US, 09/480, 977
PRIOR APPLICATION NUMBER: US, 08/899, 437
PRIOR APPLICATION NUMBER: US, 06/052, 019
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 12
LENGTH: 46
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                                                                                                                                      ) OTHER INFORMATION: Nucleotide and peptide sequence of multivalent vaccine US-10-211-994-20
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09864675
Patent No. US20020081286A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NRC-2 NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: POLYPEPTIDES, AND DIAGNOSTIC AND THERAPEUTIC METHODS
FILE REPERENCE: '04585/049002
CURRENT APPLICATION NUMBER: US/09/864,675
CURRENT APPLICATION NUMBER: US 60/206,495
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                   Score 46;
Pred. No. 4
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/10136573A Patent No. US20020161200A1
                  SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.1%;
60.0%;
                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                               Query Match 82.1%;
Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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280 CPVGYTGDRC 289
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92 CVIGYIGERC 101
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US-09-864-675-4
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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NUMBER OF SEQ
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                                                                               TYPE: PRT
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Patent No. US20020164680A1
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ExbB Receptor Specific Neuregulin Related
Ligands and Uses Therefor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 15.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/877,665
FILING DATE: 08-Jun-2001
CLASSIFICATION CURNOWN-
PRIOR APPLICATION WHORER: US/09/109,206
FILING DATE: 30-Jun-1998
ATTORNEY/AGENT INFORMATION:
NAME: COOLSY, DEITGRE L.
REFERENCE/DOCKET NUMBER: 36.487
REFERENCE/DOCKET NUMBER: 36.487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-215-862-12
; Sequence 12, Application US/10215862
; Publication No. US20030036166A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 46 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1-46
IDENTIFICATION METHOD:
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60.0%;
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COMPUTER READABLE FORM:
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Gaps
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                                                                                                             Length 46;
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gearing, David P.
Busfleld, Samantha J.
TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
2.8;
                                                                                                         Score 45; DB 10;
Pred. No. 2.7;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07334/022001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTHARE: FASTEM: DOS
SOFTHARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,241
FILING DATE: 12-Mar-2002
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/699,591
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Frankiin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND USES THEREFOR
                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-817-647-12
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-096-241-17
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/10096241 Patent No. US20020127594A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 13, Application US/10201945
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SEQUENCE CHARACTERISICS:
LENGTH: 47 amino acids
          IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                           80.4%;
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                                                                                                         Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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US-10-201-945-13
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APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie Rose
APPLICANT: Zhang, Dong Xiao
TITLE CANT: Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: PIOBARID2C1
CURRENT APPLICATION NUMBER: 2012/215,862
CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 09/126,663
PRIOR APPLICATION NUMBER: US 08/899,437
PRIOR APPLICATION NUMBER: US 08/899,437
PRIOR APPLICATION NUMBER: US 06/052,019
PRIOR PILING DATE: 1997-07-24
PRIOR PILING DATE: 1997-07-24
PRIOR PILING DATE: 1997-07-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9; Length 46;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 26-Mar-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligands and Uses Therefor
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APPLICATION NUMBER: 09/107,979
FILING DATE: CUNROWN>
ATTORNEY/AGENT INFORMATION:
NAME: CONLEY, Deitdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     80.4%; Score 45; 60.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No
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ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09817647
Patent No. US20020082229A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 12:
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1-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
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                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 23
SEQ ID NO 12
LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 CVVGYIGERC 41
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
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Matches 6; Conserv
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APPLICANT: Bilodeau-Goesseels, Sylvie
APPLICANT: John, Sushil J.
APPLICANT: Selinger, Leonard B.
APPLICANT: Benkel, Bernhard F.
TITLE OF INVENTION: Nucleic acid and protein sequences of bovine epidermal growth
TITLE OF INVENTION: factor
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DATABASE ENTRY DATE: 1993-04-21
RELEVANT RESIDUES: Relevant residues FROM 970 TO 1022
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS: Bell, G.I., Fong, N.M., Stempien, M.M., Wormsted, M.A., AUTHORS: Caput, D., Ku, L.L., Urdea, M.S., Rall, L.B. and Sanchez-AUTHORS: Pescador, R.
TITLE: Human epidermal growth factor precursor: cDNA sequence, TITLE: expression in vitro and gene organization.
                                                                                                                              : LOCATION: (0)...(0)
; OTHER INFORMATION: Epidermal Growth Factor (EGF, mature peptide)
US-09-903-327A-9
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                                                                                                                                                                                                                  Length 53;
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                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 60-01
CURRENT APPLICATION NUMBER: US/10/150,648B
CURRENT APPLICATION NUMBER: US/10/150,648B
CURRENT FILING DATE: 2002-05-17
PRIOR PELLING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
LENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ed. No. 3.1;
Mismatches
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                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.4%; Score 45; 60.0%; Pred. No.
                                                                                                                                                                                                                  Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 35, Application US/10150648B Publication No. US20030059802Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10211994
Publication No. US20030082201A1
GENERAL INFORMATION:
APPLICANT: Reo, M.R.S.
APPLICANT: Sengupta, Paromita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL: Nucleic Acids Research
VOLUME: 14
                                                                                                                                                                                                                    80.4%;
60.0%;
                                                                                                                                                                                                Query Match
Best Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 80.4
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                   33 CVVGYIGERC 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                            NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGES: 8427-8446
                                             TYPE: PRT
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-10-211-994-4
SEQ ID NO 9
LENGTH: 53
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TITLE OF INVENTIONS BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
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                                                                                   Adams, Mark D.

TITLE OF INVENTION: Transforming Growth Factor Alpha HI
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/201,945
FILING DATE: 25-Jul-2002
CLASSIFICATION: <unhal>
                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9;
2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Brockes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF110D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEX: 301-309-8439
INFORMATION FOR SEO ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 9
Pred. No. 2.8;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/471,377
FILING DATE: 23-Dec-1999
APPLICATION NUMBER: 08/915,096
FILING DATE: <UNMBER: 08/915,096
FILING DATE: ON-WARPINGOWN-
APPLICATION NUMBER: US 08/208,008
FILING DATE: 08-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                        APPLICANT: Meissner, Paul S. Fuldner, Rebecca A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09903327A Patent No. US20020164333A1 GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 48 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.4%;
US20020188110A1
                                                                                                                                                                                                                                                                               ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 80.4
Best Local Similarity 60.0
Matches 6; Conservative
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28 CVVGYIGERC 37
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                                                                                                                                                                                                                                                               USA
                      GENERAL INFORMATION
                                                                                                                                                                                                                                           STATE: MD
  Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-201-945-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-903-327A-9
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## APPLICANT: Prasad, Sudhanand
## APPLICANT: Burman, Anand C.
## APPLICANT: Burman, Anand C.
## APPLICANT: Burman, Anand C.
## APPLICANT: MULTIVALENT SYNTHETIC VACCINE FOR CANCER
## TILE REPERBENCE: 1014152-1
## CURRENT APPLICATION NUMBER: 105/10/211,994
## CURRENT APPLICATION NUMBER: 60/309,975
## PRIOR APPLICATION NUMBER: 60/309,975
## PRIOR PLICATION DATE: 2001-08-03
## PRIOR FILING DATE: 2001-08-03
## NUMBER OF SEQ ID NOS: 29
## SEQ ID NO 4
## LENGTH: 53
## LENGTH: 53
## CORGANISM: Unknown
## FEAUTRE: OTHER INPORMATION: Description of Unknown Organism: Epidermal growth factor
## Ouery Match
## Good State of Conservative State
```

Search completed: July 2, 2003, 07:57:18 Job time : 103 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

2, 2003, 07:25:01 ; Search time 12 Seconds July Run on:

(without alignments)
80.112 Million cell updates/sec US-09-673-785D-9 56

1 CVIGYSGDXC 10 Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

summaries Maximum Match 100% Listing first 45 su

PIR_73:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPTES

Result		a Query	•		SUMMARIES	
No.	Score	Match	h Length	88	QI	Description
7	26	100.0			EGMSMG	epidermal growth f
7	51	91.1	1 2139	•	A35672	
m	51	91.1			T09070	probable tenascin
4	49	87.			B55885	chondroitin sulfat
ហ	49	87.			T29359	hypothetical prote
9	49	87.5			843922	~~
7	49	87.5			T14274	Ω
œ	49	87.			A60979	
σ	49	87.			T42389	versican precursor
10	46	82.1			PC4415	ErbB kinase activa
11	46	82.]	7		EGRT	epidermal growth f
12	46	82.			T42218	slit-1 protein hom
13	45	80.4			A31246	neurogenic protein
14	45	80.4			S19087	gene Delta protein
12	45	80.4			800670	neurogenic repetit
16	45	80.4			S49126	brevican precursor
17	45	80.4			EGHU	epidermal growth f
18	45	80.4	1 1722	7	E89753	
19	45	80.4			A55535	versican precursor
20	44	78.6			T16271	hypothetical prote
21		78.6			A40136	fibropellin Ia - s
22	44	78.6			A49175	Motch B protein -
23	44	78.6			T30201	Notch homolog prot
54	44	78.6			A49128	cell-fate determin
25	44	78.6			T34022	zonadhesin - piq
56	44	78.6			A40701	tenascin-X precurs
27	44	78.6		~	T42629	tenascin-X - bovin
28	43	76.8	3 373	7	T22300	hypothetical prote
53	43	76.8		~	S78549	notch3 protein - h

hypothetical prote	probable laminin a	epidermal growth f	hypothetical prote	brevican - human (adhesive plaque pr	hypothetical prote	brevican precursor	brevican precursor	gene serrate prote	MEGF5 protein - ra	notch 3 protein -	notch homolog - se	metalloproteinase	hypothetical prote	ATP-dependent perm
T23433	T3/316	S17294	B69300	T46256	A56175	T25424	S57653	A54423	S16148	T13953	S45306	T31070	S71352	T29234	S19421
7	7	7	~	7	7	7	7	0	7	7	7	7	7	~	7
3672	3704	53	57	330	473	548	. 883	912	1408	1523	2318	2531	597	919	1049
76.8	9.0	2.0	5.0	5.0	5.0	5.0	75.0	5.0	5.0	5.0	5.0	5.0	3.2	3.2	3.2
7	_	7	7	7	7	7	7	7	7	7	7	7	7	7	7
43	4.	42	42	42	42	42	42	42	42	42	42	42	41	41	41
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
epidermal growth factor precursor - mouse
Nylternate names: urogastrone precursor
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Daccession: A94272; A93304; A92118; A01187
R;Scott, J.; Urdea, M.; Quiroga, M.; Sanchez-Pescador, R.; Fong, N.; Selby, M.; Rutt Science 221, 236-240, 1983
A;Title: Structure of a mouse submaxillary messenger RNA encoding epidermal growth f A;Reference number: A94272; MUID:83223630; PMID:6602382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Residues: 1-1217 <SCO>

A Residues: 1-1217 <SCO>

A Residues: 1-1217 <SCO>

A Gray, A.; Dull, T.; Ullrich, A.

Nature 303, 722-725, 1983

A Fitter Note of Equation of Equat
RESULT 1
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A Fincher Line Sequence shown by Liese authors there are the concern of Scott et al.)

R; Savage Jr., C.R.; Inagami, T.; Cohen, S.

J. Balol. Chem. 247, 7612-7621, 1972

A; Title: The primary structure of epidermal growth factor.

A; Reference number: A92118; MUID:73048516; PMID:4636327

A; Reference number: A92118; MUID:73048516; PMID:4636327

A; Reference number: A92118; MUID:73048516; PMID:4636327

A; Residues: 977-1029 <SAV>

A; Residues: 977-1029 <SAV>

A; Residues: 197-1029 <SAV>

A; Residues: 197-1029 <SAV>

A; Reference number: A92144; MUID:7405498; PMID:4750422

A; Reference number: A92144; MUID:74055498; PMID:4750422

A; Reference number: Bpidermal growth factor (EGF) stimulates the proliferation and differentif gastrointestinal cell proliferation; disulfide bonds

C; Comment: Epidermal growth factor (EGF) stimulates the proliferation and differentif gastrointestinal cell proliferation in the pancreas, small intestine, mammary gland, and (in gc: Comment: The EGF precursor is found in kidney as a receptor-like membrane-bound proc; Comment: The EGF precursor is found in kidney as a receptor-like membrane-bound proc; Comment: The active growth factor from this submaxillary gland protein stimulates

C.Superfamily: epidermal growth factor precursor; EGF homology; LDL receptor YWTD-co C.Keywords: duplication; growth factor; tandem repeat; transmembrane protein F:1-29-40 Domain: signal sequence #status predicted <SIG>
F:29-1217/Product: epidermal growth factor proprotein, membrane-bound form #status p F:59-1038/Domain: extracellular #status predicted <EXT>
F:50-467/Region: EGF precursor long repeat
F:53-92/Domain: LDL receptor YWTD-containing repeat homology <YW01>
F:93-134/Domain: LDL receptor YWTD-containing repeat homology <XW02>

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C. Accession: T09070
R. Rocession: T09070
R. Rocess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 124/1; 735/1; 773/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 144@/1; 019/1; 3115/1; 3208/1; 3302/1; 3405/1; 3517/1; 3558/1; 3606/1; 3646/1; 3694/1; 3737/3 C; Superfamily: tenascin-x; EGF homology; fibrinogen beta/gamma homology; fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 19-0ct-1995 #sequence_revision 19-0ct-1995 #text_change 16-Jul-1999
C:Accession: B55885
R;Zako, M.; Shinomura, T.; Ujita, M.; Ito, K.; Kimata, K.
J. Biol. Chem. 270, 3914-3918, 1995
A;Title: Expression of PG-M(V3), an alternatively spliced form of PG-M without a cond A;Reference number: A55885; MUID:95181355; PMID:7876137
A;Accession: B55885
A;Status: preliminary
A;Accession: B5885
A;Resiones: 1-102 < ZaK>
A;Resiones: 1-102 < ZaK>
A;Resiones: 1-102 < ZaK>
A;Resiones: 1-102 < ZaK>
A;Coss.references: GB:S75879; GB:D32039
C;Superfamily: versican; C-type lectin homology; complement factor H repeat homology; F;24-55/Domain: EGF homology < EG2>
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                                          probable tenascin X - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein R05G6.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: extracellular matrix
F; 422-448/Domain: EGF homology <EGF>
F; 826-906/Domain: fibronectin type III repeat homology <3FR>
F; 3789-3997/Domain: fibrinogen beta/gamma homology <FEGS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chondroitin sulfate proteoglycan MV3 - human (fragment)
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submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid R05G6
A;Reference number: 220612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.1%; Score 51; DB 2; 70.0%; Pred. No. 2.7; Live 2; Mismatches
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80.0%; Pred. No. 0.18;
tive 1; Mismatches
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Best Local Similarity 70.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 87.5
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541
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532 CAVGYSGDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: TNX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fi616-653/Domain: LDL receptor YWTD-containing repeat homology <YW10>
Fi660-700/Domain: LDL receptor YWTD-containing repeat homology <YW11>
Fi701-743/Domain: LDL receptor YWTD-containing repeat homology <YW12>
Fi711-786/Domain: LDL receptor YWTD-containing repeat homology <W12>
Fi711-743/Domain: EGF homology <EG5>
Fi842-875/Domain: EGF homology <EG6>
Fi842-875/Domain: EGF homology <EG8>
Fi923-958/Domain: EGF homology <EG8>
Fi921-1018/Domain: EGF homology <EG8>
Fi921-1018/Domain: EGF homology <EG9>
Fi932-1063/Domain: EGF homology <EG9>
Fi939-1063/Domain: IGF homology <EG9>
Fi939-1063/Domain: Intracellular #status predicted <IMT>
Fi96-127/Domain: Intracellular #status predicted <IMT>
Fi36-137/J37-386,388-401,407-418,414-427,429-442,445-457,453-467,469-482,751-76
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A; Residues: 1-2139 <TEP>
A; Cross-references: GB:M33753
A; Cross-references: GB:M33753
A; Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residu C; Genetics:
A; Mote: the authors translated proteins; EGF homology
A; Cross-references: FlyBase:FBgn000368
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Keywords: transmembrane protein
F; 352-385/Domain: EGF homology <EGF1>
F; 352-424/Domain: EGF homology <EGF2>
F; 651-722/Domain: EGF homology <EGF2>
F; 661-722/Domain: EGF homology <EGR3>
F; 1878-1914/Domain: EGF homology <EGR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Drosophila melanogaster
C:Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 11-Jan-2000
C.Species: 01-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 11-Jan-2000
C.Specesson 11-Jan-2000
C.Species 11-Jan-2000
C.Spec
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YWTD-containing repeat homology <YW03>
YWTD-containing repeat homology <YW04>
YWTD-containing repeat homology <YW05>
YWTD-containing repeat homology <YW05>
#status atypical <EG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <YW09>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;982-996,990-1007,1009-1018/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2139;
                                                                                                                                                                                                                                                                                                                                                                        WWID-containing repeat homology YWTD-containing repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Pred. No. 0.12;
1; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crumbs protein - fruit fly (Drosophila melanogaster)
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Pred. No. 1.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 56;
                                                                                                                                                                                                                                                                                                                                               long repeat
                                                                                                                                                                                                              <EG2>
                                                                                                                                                                                                                                                                                               <EG4>
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70.0%;
                                                                                                                                                                                                                                                                                                                                          precursor
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homology
homology
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Matches 9; Conservative
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Best Local Similarity
7; Conserve
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571 CAVGYSGDRC
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EGF
EGF
EGF
LDL
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                             F;486-961/Region:
F;489-529/Domain:
F;530-572/Domain:
                                                                                     :218-262/Domain:
                                                                                                                            07/Domain:
                                                                                                                                                                   324-360/Domain:
                                                                                                                                                                                                     366-401/Domain:
                                                                                                                                                                                                                                                                                               445-482/Domain:
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A; Accession: T29359

RESULT 3

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Gaps

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N;Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteogly
                                                                                                                                                                                                                                                                                                                                                                                                                                              N. Contains: gilain hyaluronate binding protein
C; Species: Homo sapiens (man)
C; Accession: S06014; S43921; A60979; A30358; A29348; A45131; I54179
E; Zimmermann, D. R.; Rucelahti, E
E; Z405-2991, 1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C; Accession: S06014; MUD: 90059882; PMID: 2583089
A; Title: Multiple domains of the large fibroblast proteoglycan, versican.
A; Reference number: S06014; MUD: 90059882; PMID: 2583089
A; Role: Li Moody, C; Schoenherr, E; Wight, T.N.; Sandell, L.J.
A; Ratix Biol. 14, Z13-Z55, 1994
A; Title: Identification of the proteoglycan versican in aorta and smooth muscle cell.
A; Reference number: Schoenherr, E; Wight, T.N.; Sandell, L.J.
A; Accession: S40921
A; Accession: S40921
A; Accession: S40921
A; Molecule type: mRNA
A; Residues: 208-440;1094-1385;1910-2246 < Xa>
A; Molecule type: mRNA
A; Residues: 208-440;1094-1385;1910-2246 < Xa>
A; Molecule type: many
A; Residues: 208-440;1094-1385;1910-2246 < Xa>
A; Molecule type: many
A; Residues: 208-440;1094-1385;1910-2246 < Xa>
A; Molecule type: many
A; Residues: 208-440;1094-1385;1910-2246 < Xa>
A; Molecule type: many
A; Residues: 208-440;1094-1385;1910-2246 < Xa>
A; Molecule type: protein
A; Residues: 171-210;289-303 < AGC
A; Residues: 171-210;289-303 < AGC
A; Residues: 171-210;289-303 < AGC
A; Residues: 24-50;80-87 < Agustal A; Accession: Adorsa
A; Residues: 24-50;80-87 < Agustal A; 
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A;Reference number: 154179
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 251-347 <RES>
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                                         ;
                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    N; Contains: glial hyaluronate-binding protein
                                     Score 49;
Pred. No. 2
                                     87.5%;
80.0%;
                                                                                                  Conservative
                                                                                                                                                                                             1362 CVPGYSGDRC 1371
                                                                                                                                                              1 CVIGYSGDXC 10
                                                                                                                                                                                                                                                                                                                                                                              versican precursor - human
                                     Query Match
Best Local Similarity
Matches 8; Conserv
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C.Keywords: glycoprotein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-1643/Product: versican, splice form V2 #status predicted <MAI>
F:21-1643/Product: versican, splice form V2 #status predicted <AMAI>
F:57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent) #st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: versican; C-type lectin homology; complement factor H repeat homology; Eq C; Keywords: chondroltin sulfate proteoglycan; extracellular matrix E; 1-37/Domain: link protein repeat homology (fragment) <LNK1> F; 58-139/Domain: link protein repeat homology <LNK2> F; 722-753/Domain: EGF homology <EG1> F; 722-753/Domain: EGF homology <EG2> F; 760-791/Domain: EGF homology <EG2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Yao, L.Y.; Moddy, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
A;Title: Identification of the proteoglycan versican in aorta and smooth muscle cells
A;Reference number: S43921; MUID:95005762; PMID:7921538
A;Accession: S43922
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A;Cross-references: EMBL:AF060458; NID:93253303; PID:93253304; PIDN:AAC24360.1
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-372 <MUR>
A;Cross-references: EMBL:U58746; PIDN:AAB00626.1; GSPDB:GN00022; CESP:R05G6.9
A;Experimental source: strain Bristol N2; clone R05G6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            versican - pig-tailed macaque (fragments)
N;Alternate names: chondroitin sulfate proteoglycan
C;Species: Macaca nemestrina (pig-tailed macaque)
C;Date: 06-Dec_1996 #sequence_revision 06-Dec-1996 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                            Length 372;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                            0.61;
                                                                                                                                                                                                                                                                                                            Score 49; DB 2
Pred. No. 0.61;
2; Mismatches
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80.0%; Pred. No. 1.4;
Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-23;234-525;526-862 <YAO>
A;Cross-references: EMBL: S72413
A;Note: 507-Ser was also found
                                                                                                                                                                                    A;Gene: CESP:R05G6.9
A;Map position: 4
A;Introns: 80/1; 161/1; 245/1; 286/1
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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Gaps

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Length 57; Indels

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epidermal growth factor precursor - rat
NAlternate names: urogastrone precursor
C.Species: Rattus norvegicus (Norway rat)
C.Date: 31-Dec-1988 #sequence_revision 14-Aug-1998 #text_change 18-Jun-1999
C.Species: 805074; 801974; A25425; S18419; S08288
R.Sagti, S.J.; Safirstein, R.; Price, P.M.
DNA Cell Biol. 11, 481-487, 1992
A.Title: Cloning and Sequencing of the Rat Preproepidermal Growth Factor CDNA: Comgar
A.Reference number: 152995; MUID:92398779; PMID:1524680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Comment: EGF is released in the pancreas, small intestine, mammary gland, and (in s C; Comment: The EGF precursor is found in kidney as a receptor-like membrane-bound pro C; Superfamily: epidermal growth factor precursor; EGF homology; LDL receptor WWTD-con C; Keywords: duplication; growth factor; mitogen; tandem repeat; transmembrane prote. F:1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 974-1024 VNEX>
C; Comment: Epideral growth factor (EGF) stimulates the proliferation and different a
gastrointestinal cell proliferation.
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A Residues: 974-1021 <SI23-
RENISBI, N.; Shimizu, C.; Okutani, T.; Ragawa, Y.; Takasuga, H.; Suno, M.; Wada, F.
Biochim. Biophys. Acta 1095, 268-275, 1991
A Fittle: Rat prostatic growth factors: purification and characterization of high ani
A; Reference number: $18419; MUID:92069070; PMID:1958699
                                ating the differentiation of MDA-MB-453 cells.
C;Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology
F;1-25/Domain: EGF homology (fragment) <EGF>
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A; Mosiduce: 'W', '956, 'RWL', '970-1023,' NW', 1026-1108,' SGAGVSSGPQPWFVVLE', 1126,' HQ' < A; Mosiduce: EMBL:X12748
A; Cross-references: EMBL:X12748
R; Dorow, D.S.; Simpson, R.J.
R; Dorow, D.S.; Simpson, R.J.
Nucleic Acids Res. 16, 9338, 1988
A; Title: Cloning and sequence analysis of a cDNA for rat epidermal growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-1133 <RES>
A;Cross-references: EMBL:U04842; NID:9440236; PIDN:AAB60436.1; PID:9440237
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A; Residues: W', 966, TRML', 970-1023, 'NW', 1026-1108 <DOR>
A; Cross-references: EMBL: X12748
EM: Simpson, R.J.; Smith, J.A.; Moritz, R.L.; O'Hare, M.J.; Rudland, Eur. J. Blochem. 153, 629-637, 1985
A; Title: Rat epidermal growth factor: complete amino acid sequence. A; Reference number: A25425; MUID: 86081810; PMID: 3000782
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A; Molecule type: protein
A; Mesidues: 974-1021 < NIS>
R; Nexo, E.; Jorgensen, P.E.; Thim, L.; Roepstorff, P.
Biochim, Biophys, Acta 1037, 388-393, 1990
A; Title: Purification and characterization of a low and A; Reference number: $89288; MUID:90181442; PMID:2310752
                                                                                                                                                                                                              82.1%; Score 46; DB 2;
llarity 60.0%; Pred. No. 0.34;
Conservative 3; Mismatches
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                        1 CVIGYSGDXC 10
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les 6; Conserv
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Best Local S
Matches 6)
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C; Accession: T42389
R; Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
J. Biol. Chem. 273, 157584-15764, 1998
A; Reference number: Z17954; MUID:98288320; PMID:9624174
A; Reference number: Z17954; MUID:98288320; PMID:9624174
A; Reference number: Z17954; MUID:98288320; PMID:9624174
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary;
A; Molecule type: mRNA
A; Residues: BMBL:AF060456; NID:93253299; PID:93253300; PIDN:AAC24358.1
C; Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin C; Reywords: chondroitin sulfate proteoglycan; extracellular matrix; glycoprotein F; 1-20/Domain: signal sequence #status predicted <515.
F; 21-3381/Product: versican, splice form VO #status predicted <MAT>
F; 21-3381/Product: versican, splice form VO #status predicted <AMAT>
F; 27, 331, 352, 817, 965, 1017, 1333, 1393, 1437, 1463, 1653, 1974, 2045, 2074, 2103, 2263, 2289, 2356, 26
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C:Species: Rattus norvegicus (Norway rat)
C:Species: Dobec-1997 #sequence_revision 10-bec-1997 #text_change 02-Aug-2002
C:Accession: Pc4415
R:Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyag A:Tilc: A novel brain-derived member of the epidermal growth factor family that interact A:Reference number: JC5700; MUID:98006324; PMID:9348101
A:Accession: Pc4415
A:Status: nucleic acid sequence not shown
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A;Experimental source: PC-12 cell
C;Comment: This-protein is a member of the epidermal growth factor family. It is function
                                                                                                                                                                     A Map position: 5412-5414
C; Superfamily: versican; C-type lectin homology; complement factor H repeat homology;
C; Superfamily: versican; C-type lectin homology; complement factor H repeat homology;
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 1-3409/Product: proteoglycan 24K core protein #status predicted <WAT>
F; 157-244/Domain: link protein repeat homology <LNK1>
F; 559-1654/Domain: chondrolitin sulfate attachment #status predicted <GAG>
F; 2106-2137/Domain: EGF homology <EG1>
F; 2106-2137/Domain: EGF homology <EG2>
F; 2106-2137/Domain: EGF homology <EG3>
F; 2106-2137/Domain: EGY h
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N'Alternate names: chondroitin sulfate proteoglycan
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
    GB:S52488; NID:9263313; PIDN:AAB24878.1; PID:9263314
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Pred. No. 5.1;
Mismatches 1; Indels
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Pred. No. 3.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2182-2302/Domain: C-type lectin homology <LCH>
                                                                                                                                         A;Cross-references: GDB:127873; OMIM:118661
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80.0%;
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Best Local Similarity 80.00,
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Best Local Similarity 80.0
Matches 8; Conservative
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A; Residues: 1-57 <HIG>
A;Cross-references:
C;Genetics:
                                                                                           A; Gene: GDB:CSPG2
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P.S.; Morrison, J.

a high molecular weight form

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C;Species: Drosophila melanogaster
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C;Accession: A31246; Alton, A.K.; Fechtel, K.; Kooh, P.J.; Muskavitch, M.A.T.
Genes Dev. 2, 1723-1735, 1988
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encod
A;Reference number: A31246; MUID:89196890; PMID:3149249
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C; Species: Drosophila melanogaster
C; Species: 31-Dec-1988 #text_change 02-Aug-2002
C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 02-Aug-2002
C; Accession: $00670; A26637
R; Vaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.
EMBO J. 6, 3431-3440, 1987
A; Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurog A; Reference number: $00670
A; Accession: $00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Drosophila melanogaster
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
C;Accession: S19087
s;Muskavitch, M.A.T.
submitted to the EMBL Data Library, June 1991
A;Reference number: S19087
A;Status: preliminary
A;Status: preliminary
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-833 <mrs/>
Amis, Amis
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A; Wolecule type: mRNA
A; Residues: 1-832 < kOP>
A; Cross-references: GB:Y00222
C; Genetics:
A; Gene: FlyBase:Dl
A; Cross-references: FlyBase:Fbgn0000463
C; Superfamily: neurogenic protein delta; EGF homology
F; 295-338/Domain: EGF homology < EGX1>
F; 422-450/Domain: EGF homology < EGF1>
F; 457-488/Domain: EGF homology < EGF2>
F; 533-564/Domain: EGF homology < EGF3>
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Pred. No. 6.6;
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Pred. No.
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A,Cross-references: FlyBase:FBgn0000463
C,Superfamily: neurogenic protein delta,
F,335-371/Domain: EGF homology <EGF1>
F,378-415/Domain: EGF homology <EGF2>
F,457-488/Domain: EGF homology <EGF>
F,533-564/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.4%;
70.0%;
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 |||||:|
319 CAPGYSGDDC 328
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F;22-1133/Product: epidermal growth factor proprotein, membrane-bound form #status predicts F;42-1035/Domain: extracellular #status predicted <EXT>F;44-80/Region: EGF precursor long repeat <LR1>F;47-86/Domain: LDL receptor YWTD-containing repeat homology <YW01>F;47-86/Domain: LDL receptor YWTD-containing repeat homology <YW02>F;128/Domain: LDL receptor YWTD-containing repeat homology <YW03>F;129-170/Domain: LDL receptor YWTD-containing repeat homology <WW05>F;28-302/Domain: LDL receptor YWTD-containing repeat homology <WW05>F;28-302/Domain: LDL receptor YWTD-containing repeat homology <WW05>F;313-35/Domain: LDL receptor YWTD-containing repeat homology <WW05>F;319-35/Domain: EGF homology *EG2>F;319-35/Domain: EGF homology <EG3>F;310-35/Domain: EGF homology <EG4>F;340-47/Domain: EGF homology <EG4>F;340-47/Domain: EGF procursor long repeat <LR2>F;348-255/Domain: LDL receptor YWTD-containing repeat homology <WW07>F;36-568/Domain: LDL receptor YWTD-containing repeat homology <WW08>F;56-568/Domain: LDL receptor YWTD-containing repeat homology <WW09>F;56-568/Domain: LDL receptor YWTD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1036-1060/Domain: transmembrane #status predicted <TMM>
F;1061-1133/Domain: intracellular #status predicted <INT>
F:342-335,361-372,368-381,383-396,402-113,409-422,424-437,440-452,448-462,464-477,747-75-1015/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rinakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: 214126; MUID:98360089; PMID:9693030
A;Accession: T42218
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: MEGF4
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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A;Residues: 1-1531 <NAK>
A;Cross-references: EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3449290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth factor #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <YW10>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.1%; Score 46; DB 1; Length 1133; 70.0%; Pred. No. 6;
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homology
homology
homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor YWTD-containing repeat receptor YWTD-containing repeat
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Best Local Similarity 70.0%; Pred. No. 8;
Matches 7; Conservative 2; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDL receptor YWTD-co
LDL receptor YWTD-co
LDL receptor YWTD-co
EGF homology <EG5>
EGF homology <EG6>
EGF homology <EG6>
EGF homology <EG6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;979-1015/Domain: EGF homology <EG9>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.1
Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1071 CVPGYTGDNC 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CVIGYSGDXC 10
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A:Wolecule type: mRNA
A:Residues: 1-880 <VAE>
A:Residues: 1-880 <VAE>
A:Cross-references: EMBL:X06289; NID:97852; PID:97853
B:Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ort EMBO J. 6, 761-766, 1987
A:Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and A:Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and A:Reference number: A91081; MUID:87218537; PMID:3107986
A:Accession: A26637
A:Molecule type: mRNA
A:Residues: 422-436, ET', 439-458, A', 460-489, T', 491-621 <KNU>
A:Residues: 422-436, ET', 439-458, B':A', 460-489, B':A', 491-621 <KNU>
A:Cross-references: GB:X05140; NID:97851; PIDN:CAA28786.1; PID:9929563
                                                                                                                                                                                                                                                                                                                                                                                                                    Glonetics:
A;Gene: Delta; Dl
A;Gene: Delta; Dl
A;Gene: Delta; Dl
A;Gene: Delta; Dl
C;Seyvords: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein
C;Seyvords: transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>
F;333-564/Domain: EGF homology <EGF1>
F;533-564/Domain: EGF homology <EGF2>
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80.4%; Score 45; DB 2; Length 880;
Best Local Similarity 70.0%; Pred. No. 7;
Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: July 2, 2003, 07:26:26 Job time : 12 secs
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319 CAPGYSGDDC 328
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July 2, 2003, 07:25:02; Search time 10.3333 Seconds (without alignments) 40.138 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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56
1 CVIGYSGDXC 10
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Maximum DB seq length: 200000000
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                                                                                                                                                                               Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

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	ption	mus musculu	drosophila	macaca neme	bos taurus	homo sapien	mus musculu	mus musculu	rattus norv	drosophila	rattus norv	homo sapien	rattus norv	rattus norv	mus musculu	strongyloce	mus musculu	homo sapien	rattus norv	sus scrofa	homo sapien	homo sapien	caenorhabdi	sus scrofa	archaeoglob	mytilus gal	mus musculu	bos taurus	drosophila	mus musculu	paracentrot	saccharomyc	mus musculu	brachydanio
	Description	P01132	P10040	028858	P81282	P13611	Q9r0m0	P56974	P07522	P10041	P55068	P01133	Q9r172	Q9erb4	062059	P10079	035516	004721	08wb60	028983	P22105	Q9um47	Q21313	896000	029845	025464	061361	028062	P18168	Q61982	P42674	P25371	061092	P46530
SUMMARIES	CI CI	EGF_MOUSE	CRB_DROME	PGCV_MACNE	PGCV_BOVIN	PGCV_HUMAN	CLR2_MOUSE	NRG2_MOUSE	EGF_RAT	DL_DROME	PGCB_RAT	EGF_HUMAN	NTC3_RAT	PGCV_RAT	PGCV_MOUSE	FBP1_STRPU	NTC2_MOUSE	NTC2_HUMAN	NTC2_RAT	ZAN_PIG	TENX_HUMAN	NTC3_HUMAN	LML2_CAEEL	EGF_PIG	Y402_ARCFU	FP2_MYTGA	PGCB_MOUSE	PGCB_BOVIN		NTC3_MOUSE	BP10_PARLI	ADP1_YEAST	- 1	NTC1_BRARE
	DB	; -	٦	Н	П	-	г	7	-	н	Н	-	-	Н		Н	-	-	-	-	-	Н	Н	-	Н	Н	Н	-	Н	-	Н		-	
	Query Match Length	1217	2139	862	3381	3396	2920	156	1133	833	883	1207	2319	2738	3358	1064	2470	2471	2471	2476	4289	2321	3672	23	57	473	883	912	1408	2318	597	1049	1192	2437
df	Query Match	100.0	ä	87.5	87.5	87.5	85.7	82.1	82.1	80.4	80.4	80.4	80.4	80.4																		73.2		73.2
	Score	56	51	49	64	49	48		46										44		44	43	43	42	42	42	42	42	42	42	41	41	41	41
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3.4	40	71.4	427	П	MFGM_RAT	P70490	rattus norv
35	40	71.4	463	Н	MFGM_MOUSE	P21956	mus musculu
36	40	71.4	723	П	DLL1_HUMAN	000548	homo sapien
37	40	71.4	1213	٦	JAG3_BRARE	Q90y54	brachydanio
38	40	71.4	1218	Н	JAG1_HUMAN	P78504	homo sapien
39	40	71.4	1218	П	JAG1_MOUSE	099xx0	mus musculu
40.	40	71.4	1219	Н	JAG1_RAT	063722	
41	40	71.4	1242	Н	JAG1_BRARE	Q90y57	
42	40	71.4	1429	7	LI12_CAEEL	P14585	caenorhabdi
43	40	71.4	2531	7	NTC1_MOUSE	001705	_
44	40	71.4	2531	Н	NTC1_RAT	00700	rattus norv
45	40	71.4	2703	Н	NOTC_DROME	P07207	drosophila
							,
					ALIGNMENTS		
ESULT 1							

1	EGF_MOUSE STANDARD; PRT; 1217 AA.
	P01132; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Pro-epidermal growth factor precursor (EGF) (Contains: Epidermal
	EGF. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
	[1] MEDLINE-83223630; PubMed-6602382; SEQUENCE FROM N.A. SCOLT J., Urdea M., Quiroga M., Sanchez-Pescador R., Fong N.M., Selby M., Rutter W.J., Bell G.I.; "Structure of a mouse submaxillary messenger RNA encoding epidermal growth factor and seven related proteins."; Science 221:236-240(1983).
	SEQUENCE FROM N.A. MEDLINE-83219309; Pubmed-6304537; Gray A., Dull T.J., Ullrich A.; "Nuclectide sequence of epidermal growth factor cDNA predicts a 128,000-molecular weight protein precursor."; Nature 303:722-725(1983).
	15] MEDLINE-73048516; PubMed-4636327; MEDLINE-73048516; PubMed-4636327; Savage C.R. Jr., Inagami T., Cohen S.; "The primary structure of epidermal growth factor."; J. Biol. Chem. 247:7612-7621(1972).
	<pre>14) InsulrIDE BONDS. MEDLINE=74025498; PubMed=4750422; Savage C.R. Jr., Hash J.H., Cohen S.; "Epidermal growth factor. Location of disulfide bonds."; J. Biol. Chem. 248:7669-7672(1973).</pre>
	MEDLINE-92118798; PubMed-1731873; MEDLINE-92118799 PubMed-1731873; Montalione G.T., Wathrich K., Burgess A.W., Nice E.C., Wagner G., Gibson K.D., Scheraga H.A.; "Solution structure of murine epidermal growth factor determined by NMR spectroscopy and refined by energy minimization with Erestraints."; Biochemistry 31:236-249(1992).
	loj STRUCTURE BY NMR OF 977-1029. MEDLINE-93075811; PubMed-1445923; Kohda D., Inagaki F.; "Three-dimensional nuclear magnetic resonance structures of mouse

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NOT REQUIRED FOR FULL BIOLOGICAL ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-Oregon-R; TISSUE-Embryo;
MEDLINE-90263104; PubMed-2344615;
Tepass U., Theres C., Knust E.;
"Crumbs encodes an EGF-like protein expressed on apical membranes of procephila epithelial cells and required for organization of epithelia".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                             IN VIVO.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

D -> Y (IN REF. 2).

A -> S (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Embryo;
MEDLINE-87218537; PubMed-3107986;
Knust E., Dietrich U., Tepass U., Bremer K.A., Weigel D.,
                                                                                                                                                                                                                                                                                                                                             133144 MW; A9C7F3D512F82873 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
10-MAY-1991 (Rel. 18, Last sequence update)
10-JUN-2002 (Rel. 41, Last annotation update)
Crumbs protein precursor (95F).
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  SEQUENCE OF 1663-1955 FROM N.A.
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Cell 61:787-799(1990).
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Matches 9; Conserv
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                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               STRUCTURE BY NAMR OF 980-1024.

MEDLINE-99180407; Pubmed-10082370;
Barnham K.J., Torres A.M., Alewood D., Alewood P.F., Domagala T.,
Nice E.C., Norton R.S.;

"Role of the 6-20 disulfide bridge in the structure and activity of epidermal growth factor.";
"Role of the 6-20 disulfide bridge in the structure and activity of epidermal growth factor.";
"In protein Sci. 7:1738-1749(1998).

"Protein Sci. 7:1738-1749(1998).

"In PROPINENT IN CELL CULTURE. IN VIVO AND IN VITRO AND OF SOME FIRROBLASTS IN CELL CULTURE.

"SUBCELLULAR LOCATION: Type I membrane protein."

"SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.

"TO 1168 DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1 (INCOMPLETE).
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
EGF-LIKE 9.
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BY SIMILARITY.
BY SIMILARITY.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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EMBL; V00741; CAA24115.1; ALT_FRAME.
EMBL; V00741; CAA24116.1; -.
PIR; A01387; EGMSMG.
Biochemistry 31:11928-11939(1992)
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PDB; 3EGF; 31-JAN-94
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Gaps

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LAMININ G-LIKE 3.

EGF-LIKE 2.

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POTENTIAL.

EGF-LIKE 1.

EGF-LIKE 3.

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(POTENTIAL).
A Vaessin H., Campos-Ortega J.A.;

"EGF homologous sequences encoded in the genome of Drosophila
T melanogaster, and their relation to neurogenic genes.";

"EMBO J. 6.761-766(1987).
"C -1- FUNCTION: MAY PLAY A ROLE IN THE DEVELOPMENT OF EPITHELIA,
DOSSIBLY FOR THE ESTABLISHMENT AND/OR MAINTENANCE OF CELL
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

"C -1- STMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
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LAMININ G-LIKE 2.
EGF-LIKE 21.
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C-TYPE LECTIN.

BY SIMILARITY.

BY S
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SIMILAR TO CHONDROITIN SULFATE ATTACHMENT
SITE IN COLLAGEN TYPE IX (BY SIMILARITY).
      SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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SMART; SMO019; EGF_CA; 1.

SMART; SMO001; EGF_LIKe; 1.

SMART; SMO001; EGF_LIKe; 1.

SMART; SMO0001; EGF_LIKe; 1.

RACSITE; PS001001; ASX_HYDROXYL; 1.

RACSITE; PS01186; EGF_L2; 1.

R PROSITE; PS01187; EGF_L3; 1.

R PROSITE; PS01241; LINK; 1.

R PROSITE; PS01041; C_TYPE_LECTIN_1; PARTIAL.

R ROSITE; PS00615; C_TYPE_LECTIN_1; PARTIAL.

R ROSITE; PS00615; C_TYPE_LECTIN_1; LINK; 1.

R GIYCOPTOCIO; Proteoglycan; Lectin; Extracellular matrix; Repeat; M GIYCOPTOCIO; TRE domain; Calcium.
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LINK 2.
GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
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Pred. No. 0.35;
1; Mismatches
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InterPro; IPR000561; EGF-11ke.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Lectin_C.
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95583 MW;
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80.0%;
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ProDom; PD000918; Link; 2
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TISSUE-Abortic smooth muscle;

MEDLINE-95005762; PubMed-7921538;

MEDLINE-95005762; PubMed-7921538;

MEDLINE-95005762; PubMed-7921538;

MEDLINE-95005762; PubMed-7921538;

Tidentification of the proteoglycan versioan in aorta and smooth muscle cells by DNA sequence analysis, in situ hybridization and immunohistochemistry. ;

Matrix Biol. 14:213-225(1994).

I FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds
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PGCV_MACNE STANDARD; PRT; 862 AA.

Q28859; Q28860;
Q1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Versican core protein (Large fibroblast proteoglycan) (Chondroitin Sulfate proteoglycan core protein 2) (Fragments).

CSPG2.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
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SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 2 LINK DOMAINS.
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Pred. No. 0.37;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blochim. Blophys. Acta 1075:248-258(1991).
-I- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Spinal cord;
MEDLINE-92062692; PubMed-1720020;
Perides G., Biviano F., Bignami A.;
"Interaction of a brain extracellular matrix protein with hyaluronic acid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zimmermann D.R.;
"Versican V2 is a major extracellular matrix component of the mature
bovine brain.";
J. Biol. Chem. 273:15758-15764(1998).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                           PGCV_BOVIN STANDARD; PRT; 3381 AA.
P81282; 077609; 077610; 077612;
15-DEC-1998 (Rel. 37, ceated)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2010 (Rel. 41, Last annotation update)
16-OCT-2011 (Rel. 41, Last annotation update)
16-UN-2010 (Rel. 41, Last annotation update)
17-UN-2010 (Rel. 41, Last annotation update)
18-UN-2010 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS VO; V1; V2 AND V3).
TISSUE-Forebrain;
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InterPro; IPR000561; EGF-11ke.
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EMBL; AF060488; AAC24360.1; -.
EMBL; AF060459; AAC24361.1; -.
HSSP; P01132; 1EPG.
Bos taurus (Bovine).
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LINK 1.
LINK 2.
GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
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SIGNAL 1 20 POTENTIAL.

CHAIN 21 3381 VERSICAN CORE PROTEIN.

DOMAIN 37 138 IG-LIKE V-TYPE DOMAIN.
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EGF-LIKE 2, CALCIUM-BINDING.
C-TYPE LECTIN.
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Pram; PP000047; 19; 1.
Pram; PP000047; 19; 1.
Pram; PP000049; 19ctin_c; 1.
Pram; PP000193; 10ctin_c; 1.
Pram; PP00193; XIInk; 2.
Propom; PP00193; XIInk; 2.
Propom; PP001918; LINKNODULE.
PRODOM; PR001918; LINKNODULE.
SMART; SM00034; CLECT; 1.
SWART; SM00179; EGF_CA; 2.
SWART; SM00179; EGF_CA; 2.
SWART; SM00449; IG; 1.
SWART; SM00440; IG; 1.
SWART; SM00445; LINK; 2.
PROSITE; PS00010; ASZ_HYRROXYL; 1.
PROSITE; PS00010; ASZ_HYRROXYL; 1.
PROSITE; PS00012; EGF_1; 2.
PROSITE; PS00012; EGF_1; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
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Sushi_SCR_CCP.
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EGF_2.
EGF_Ca.
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                                                             InterPro; IPR003006; I
InterPro; IPR003600; I
InterPro; IPR001304; L
InterPro; IPR000538; InterPro; IPR000436; S
                                          InterPro; IPR003599;
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PARTIAL SEQUENCE.
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                     (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Naso M.F., Zimmermann D.R., Iozzo R.V., "Characterization of the complete genomic structure of the human versican gene and functional analysis of its promoter.", J. Biol. Chem. 269:32999-33008(1994).
                                                                                                                                                                                                                                                                                                                      PGCV_HUMAN STANDARD, PRT, 3396 AA.
P13611, P2078-4, O9UNWS; 013010; 013189; 015123;
01-1AN-1990 (Rel. 13, created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-0GT-2001 (Rel. 40, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Gilal
                                                                                                                                                                                                                                       ;
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"A novel glycosaminoglycan attachment domain identified in two
alternative splice variants of human versican.";
J. Biol. Chem. 269:32998(1994).
N-LINKED (GLCNAC...) (POTENT MISSING (IN ISOFORM V1).

MISSING (IN ISOFORM V2).

MISSING (IN REF. 2).

MISSING (IN REF. 2).

N -> D (IN REF. 2).

C -> R (IN REF. 2).

C -> R (IN REF. 2).
                                                                                                              AND V3).
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MEDLINE-88007514; PubMed-2820964;
Krusius T., Gehlsen K.R., Ruoslahti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM V0).
MEDLINE-95105188; PubMed-7528742;
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MEDLINE=90059882; PubMed=2583089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=7806529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM V2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM V1).
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                                                                                                                                                                                               369984
                                                                                                                                                                                                                 87.5%;
                                                                                                                                                                                                                           80.08;
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                                                                                                                                                                                                                         Similarity 80.0
8; Conservative
                                                                                                                                                                                                                                                                        3100 CVPGYSGDRC 3109
                             22290
2356
2623
2641
2919
3052
3364
1336
3074
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                                                                                                                                                                                              3381 AA;
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MEDLINE=95105187; P
                   NCBI_TaxID=9606;
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CONFLICT
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to itcense@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McPharson J.D.;
"Mapping of the versican proteoglycan gene (CSPG2) to the long arm of
human chromosome 5 (5q12-5q14).";
Genomics 14:845-851(1992).
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
MEDLINE-95181355; PubMed-7876137;

ARDLINE-95181355; PubMed-7876137;

Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;

"Expression of PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and human tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-like and growth factor-like sequences."; J. Biol. Chem. 262:13120-13125(1987).
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-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
-!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lemire J.M., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Versican/PG-M isoforms in vascular smooth muscle cells.";
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perides G., Lane W.S., Andrews D., Dahl D., Bignaml A., "Isolation and partial characterization of a glial hyaluronate-bloding protein." J. Biol. Chem. 264:5981-5987(1989).
                                                                                                                          SEQUENCE OF 251-347 FROM N.A.
MEDLINE-93122792; PubMed-1478664;
IOZZO R.V., NaSO M.F., Cannizzaro L.A., Wasmuth J.J.,
McPherson J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 3333-3396 FROM N.A. (ISOFORM VINT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Aortic smooth muscle;
MEDLINE~99327053; PubMed=10397680;
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MEDLINE-89174663; PubMed-2466833;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM V3).
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Gaps

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PubMed=10790539; Pubmed=10790539; Pubmed=10790539; Pubmed=10790539; Pormstone C.J., Barclay J., Rees M., Little P.F.R.; Chromosomal localization of Celsr2 and Celsr3 in the mouse; Celsr3 is a candidate for the tippy (tip) lethal mutant on chromosome 9."; Mamm. Genome 11:392-394(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mech. Dev. 112:157-160(2002).

-!- FUNCTION: Receptor that may have an important role in cell/cell standing during nervous system formation.

-!- SUBCELLUIAR LOCATION: Integral membrane protein.
-!- DEVELOPMENTAL STAGE: Predominantly expressed in the developing CNS, the emerging dorsal root ganglia and cranial ganglia. In the CNS, expression is uniform along the rostrocaudal axis. During gastrulation, it is expressed within the anterior neural ectoderm. At El0, expression is strong in the ventricular zones (VZ) in all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usui T., Shima Y., Shimada Y., Hirano S., Burgess R.W., Schwarz T.L., Takeichi M., Uemura T.; Hirano S., Burgess R.W., Schwarz T.L., Flamingo, a seven-pass transmembrane cadherin, regulates planar cell polarity under the control of frizzled."; cell 98:585-595(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLR2_MOUSE STANDARD; PRT; 2920 AA.
09R0M0; Q922R4; Q99K26;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 2 precursor (Flamingo 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE.
PubMed=11850187;
Tissir F., De-Backer O., Goffinet A.M., Lambert de Rouvroit C.A.;
"Developmental expression profiles of Celsr (Flamingo) genes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
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Pred. No. 1.3;
1; Mismatches
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N-LINKED
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MEDLINE-99418630; Pubmed-10490098;
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80.0%;
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hes 8; Conservative
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CLR2_MOUSE
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Matches
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R PRINTS, FRO01010; EGERLOOD.

R SMART; SM00031 CCP; 1.

SMART; SM00034; CLECT; 1.

SMART; SM00015 EGF_CA; 1.

SMART; SM00016; EGF_CA; 1.

SMART; SM00445; LINK; 2.

R PROSITE; PS001016; EGF_1; 2.

R PROSITE; PS001016; EGF_2; 1.

R PROSITE; PS01186; EGF_2; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01041; CLTYPE_LECTIN_1; 1.

R PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

R PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

R PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

R PROSITE; PS01041; EGF_CA; 1.

R PROSITE; PS01041; C_TYPE_LECTIN_2; 1.
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
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SUSHI.
BY SIMILARITY.
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LINK 2.
                                                                                                                                                                                                                                                                        InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                InterPro; IPR000152; Asx_hydroxyl
EMBL, U26555, AAA67565.1; --
EMBL, D32039, BAA66801.1; --
EMBL, J02814; AAA36437.1; --
EMBL, AF084545; AAA48545.1; --
PIR, S06014; AS06014; S06014; S06014; AS06148; AS06148.
PIR, A29348; A39348.
PIR, A30358; A30358.
HSSP, P01122; IEGF.
GENEW, HGNC.2444; CSPG2.
MIM; 118661; --
                                                                                                                                                                                               InterPro; IPR000561; EGF-like
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                            Pfan; PF00008; EGF; 2.
Pfan; PF00007; 1g; 1.
Pfan; PF00059; lectin_c; 1.
Pfan; PF00084; sushi; 1.
Pfan; PF00193; X11nk; 2.
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CADHERIN 4.
CADHERIN 4.
CADHERIN 5.
CADHERIN 5.
CADHERIN 6.
CADHERIN 7.
CADHERIN 9.
EGF-LIKE 1 (ATYPICAL).
EGF-LIKE 3. CALCIUM-BINDING.
LAMININ G-LIKE 1.
EGF-LIKE 4.
CALCIUM-BINDING.
EGF-LIKE 5.
CALCIUM-BINDING.
EGF-LIKE 5.
CALCIUM-BINDING.
EGF-LIKE 6.
CALCIUM-BINDING.
EGF-LIKE 7.
CALCIUM-BINDING.
EGF-LIKE 7.
CALCIUM-BINDING.
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CALCIUM-BINDING.
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                   JOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                      Sectors of the brain, and lower in the marginal zones (MZ).
Between E12 and E15, expression is prominant in the brain. It is strong in VZ, lower in MZ, except in telecephalic MZ where it is predominant. The intensity is higher in all VZ, and lower in differenciating fields than in VZ, except in the cerebral hemispheres, and to a lesser extent in the tectum and cerebral hemispheres, and to a lesser extent in the fetal lungs, kidney and epithelia. In the newborn and postrating and postmigratory is troughout the brain.

C = 1 TISSUE SPECIFICITY: Expressed in the CNS and in the eye.

I TISSUE SPECIFICITY: Expressed in the CNS and in the eye.

SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.

SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 LAMININ GF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'ROSITE: PS50221; GPS; 1.
PROSITE: PS50025; LAM.G_DOMAIN; 2.
PROSITE: PS50025; LAM.G_DOMAIN; 2.
G-protein coupled receptor; Transmembrane; Glycoprotein;
EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
Developmental protein; Hydroxylation; Signal.
SIGNAL
CHAIN 32 2920 CADHERIN EGF LAG SEVEN-PASS G-TYPE
RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FALSE_NEG.
FALSE_NEG.
1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00022; EGF_1; 6.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS00649; G_PROTEIN RECEP_F2_1; PS00650; G_PROTEIN RECEP_F2_2; PROSITE; PS5027; G_PROTEIN RECEP_F2_2; PROSITE; PS50261; G_PROTEIN RECEP_F2_3; PROSITE; PS50261; G_PROTEIN RECEP_F2_3; PROSITE; PS50261; G_PROTEIN RECEP_F2_3; PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AB028499; BAA84070.1; -
EMBL, AF011573; AAC68937.1; -
EMBL, BE005499; AAH05499.1; -
HSSP; PO0740; 1EDM.
MGD; MGI:1858235; Celsr2.
InterPro; IPR000152; Asx Indroxyl.
InterPro; IPR000156; Cadherin.
InterPro; IPR000742; EGF.2.
InterPro; IPR000742; EGF.2.
InterPro; IPR000832; GPCR.secretin.
InterPro; IPR000832; GPCR.secretin.
InterPro; IPR000832; GPCR.secretin.
InterPro; IPR000832; GPCR.secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO01791; Laminin_Cor.
InterPro; IPRO01791; Laminin_G.
Fram; PRO0129; FRD_Cys_Tich.
Pfam; PRO0129; Cadherin; 9.
Pfam; PRO0028; Cadherin; 9.
Pfam; PRO01825; Cadherin; 9.
Pfam; PRO01825; GPS; 1.
Pfam; PRO01825; CADHERIN.
PRINTS; PRO0124; Laminin_G; 2.
PRINTS; PRO0124; Laminin_G; 2.
PRINTS; PRO011; EGFLAMININ.
PRINTS; PRO011; EGFLAMININ.
PRINTS; SMO0112; CA.9.
SMART; SMO011; CA.9.
SMART; SMO0101; EGF_Lam; 1.
PROSITE; PSO0101; ASX_HYDROXYL; 1.
PROSITE; PSO0122; CADHERIN_2; 9.
PROSITE; PSO0122; EGF_L1; 6.
PROSITE; PSO1186; EGF_L1; 6.
PROSITE; PSO1186; EGF_L1; 6.
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DOMAIN
DOMAIN
DOMAIN
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DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN (BY SIMILARITY).

PTH: PROTEDLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of a neuregulin-related gene, Don-1, that is highly expressed in restricted regions of the cerebellum and hippocampus."; Mol. Cell. Biol. 17:4007-4014(1997).

**Nol. Cell. Biol. 17:4007-4014(1997).

**PURCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS, RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND ACTIVATION OF THE ERBB RECEPTORS. MAY ALSO PROMOTE THE HETERODIMERIZATION WITH THE EGF RECEPTOR.

**INTERNATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS A PROTECLYICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).

**INTERNATIVE PRODUCTS: A LIGAST 4 ISOSORMS; DON-1M, DON-1S/ARG2-5, NRG2-10 AND NRG2-16 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pro-neuregulin-2 precursor (Pro-NRG2) [Contains: Neuregulin-2 (NRG-2) (Divergent of neuregulin 1) (DON-1)].
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Choroid plexus;
MEDLINE-97342638; PubMed-9199335;
Busfield S.J., Michnick D.A., Chickering T.W., Revett T.L., Ma J., Woolf E.A., Comrack C.A., Dussault B.J., Woolf J., Goodearl A.D.J., Gearing D.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: HIGHEST EXPRESSION IN THE BRAIN, WITH LOWER LEVELS IN THE LUNG. IN THE CEREBELLUM, FOUND IN GRANULE AND
                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
.) (POTENTIAL).
                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CS7BL/6; TISSUE-Brain; MEDIANE-9731138; PubMed-9168115; Carraway K.L. III, Weber J.L., Unger M.J., Ledesma J., Yu N., Cassmann M., Lai C., a new ligand of ErbB3/ErbB4-receptor tyrosine
                                                                                                DB 1; Length 2920;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS NRG2-5; NRG2-10 AND NRG2-16A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 150-756 FROM N.A. (ISOFORMS DON-1M AND DON-1S)
                                                                                                                      1; Indels
Score 48; DB 1
Pred. No. 1.7;
2; Mismatches
                                                                                            85.7%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 387:512-516(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORM (BY SIMILARITY).
                                                                                                                      Conservative
                                                                                                                                                           1820 CVLGYYGDNC 1829
                                                                                                                                                                                                                                STANDARD;
                         2199
2283
2535
2571
2639
                                                                                                                                             1 CVIGYSGDXC 10
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                                                                                                       Best Local Similarity
Matches 7; Conserv
 2324
2346
2199
2283
2283
2531
2639
                                                                                                                                                                                                                                NRG2_MOUSE
P56974;
                                              CONFLICT
CONFLICT
CONFLICT
                                                                                               Query Match
  CARBOHYD
             CARBOHYD
                         CONFLICT
                                    CONFLICT
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                                                                                                                                                                                                        RESULT 7
NRG2_MOUSE
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CVALLVVG -> NGFFGQRCLEKLPLRLYMPDPKQSVLMDT
PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTECLYTIC CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGTGVSSSQWSTSPSTLDLN (IN ISOFORM DON-1S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                               Pfam; pr00047; ig; 1.
Pfam; pr00047; ig; 1.
SMART; SM00181; BGF; 1.
SMART; SM00408; IGc2; 1.
PROSTIE; PS00120; EGF_1; 1.
Growth factor; EGF_1; Immunoglobulin domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Multigene family; Alternative splicing.

PROPEP
1 19 BY SIMILARITY.
CHAIN 20 756 PRO-NEUREGULIN-2, MEMBRANE-BOUND FORM.
20 315 NETRECELLURAR (POTENTIAL).
TRANSMEM 316 336 INTERNAL SEQUENCE (POTENTIAL).
DOMAIN 377 756 CYTOPELASMIC (POTENTIAL).
DOMAIN 158 226 IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
C -> G (IN ISOFORM NRG2-10).
MISSING (IN ISOFORM NRG2-10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF_RAT STANDARD; PRT; 1133 AA.
01-522 G63183;
01-78F-1988 (Rel. 07, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pro-epidermal growth factor precursor (EGF) [Contains: Epidermal growth factor].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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LPLRLYMPDPKQK (IN ISOFORM DON-1M)
51D85DC918BE678E CRC64;
                      SIMILARITY).
--- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
--- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 756;
1.1;
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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINED (GICNAC.
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EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46;
Pred. No.
                                                                                                           HSSP; Q12784; 1HRE.
MGD; MG1:1098246; Nrg2.
InterPro; IPR000561; EGF-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_C2.
InterPro; IPR002154; Neuregulin.
Pfam; PP00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         756 AA; 82213 MW;
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 : | | : | | : | 280 CPVGYTGDRC 289
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Best Local Similarity
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VARSPLIC
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EGF-LIKE 6.
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosphila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoplera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaessin H., Bremer K.A., Knust E., Campos-Ortega J.A.;
Vaessin H., Bremer K.A., Knust E., Campos-Ortega J.A.;
"The neurogenic gene Delta of Drosophila melanogaster is expressed ineurogenic territories and encodes a putative transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> S (IN REF. 4).
C224A302E9578031 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
C -> V.
KL -> NW (IN REF. 4).
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(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DL_DROME STANDARD; PRT; 833 AA. P10041; Q9VDY2; Q99108; 01-MAR-1989 (Rel. 10, Created) 16-OCT-2001 (Rel. 40, Last sequence update) Neurogenic locus Delta protein precursor. DL OR CG3619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 1
Pred. No. 1.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.1%;
70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with EGF-like repeats.";
EMBO J. 6:3431-3440(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.1
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1006 CVIGYIGERC 1015
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1025
1108
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942
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SEQUENCE FROM N.A.
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DISULFID
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DL_DROME
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                                                                                                                                                                                     SEQUENCE OF 974-1021.
MEDILINE-66081810; Pubmed=3000782;
Simpson R.J., Smith J.A., Moritz R.L., O'Hare M.J., Rudland P.S.,
Morrison J.R., iloyd C.J., Grego B., Burgess A.W., Nice E.C.;
"Rat epidermal growth factor: complete amino acid sequence. Homology
with the corresponding murine and human proteins; isolation of a form
truncated at both ends with full in vitro biological activity.";
Eur. J. Biochem. 153:629-637(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 16:9338-9338(1988).

-!- FUNCTION: THE GROWTH FACTOR STIMULATES THE GROWTH OF VARIOUS EPIDERMAL AND EPITHELIAL TISSUES IN VIVO AND IN VITRO AND OF SOME FIBROBLASI NI CELL OUTURE.

-!- SUBCELLULAR LOCATION: TYPE I membrane protein.
-!- SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1 (INCOMPLETE).
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 6.
PROSITE; PS01187; EGF_2; 6.
EGF_21tke domain; Repeat; Growth factor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and sequence analysis of a cDNA for rat epidermal growth
      MEDLINE-5238779; PubMed=1524680;
Price P.M., Saggi S.J., Safirstein R.;
"Cloning and sequencing of the rat preproepidermal growth factor
CDNA: comparison with mouse and human sequences.";
DNA Cell Biol. 11:481-487(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO-EPIDERMAL GROWTH FACTOR.
EPIDERMAL GROWTH FACTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                          TISSUE-Kidney; Price P.M.; Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U04842; AAB60436.1; --
EMBL; X12748; CAA31241.1; --
FIR; A2542; EGRT.
INTERPIO; IPR000152; Asx_hydroxyl.
INTERPIO; IPR000152; Asx_hydroxyl.
INTERPIO; IPR0001651; EGF-1ike.
INTERPIO; IPR001336; EGF-1ike.
INTERPIO; IPR001381; EGF_0.
INTERPIO; IPR001881; EGF_0.
INTERPIO; IPR000081; EGF_0.
Ffam; PF00008; Id_recept_b; 7.
Ffam; PF00008; Id_recept_b; 7.
FMINTS; FM00179; EGF_CA; 2.
SWART; SW00179; EGF_CA; 2.
SWART; SW00135; LX; 8.
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 994-1108 FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Kidney;
MEDLINE-89016634; PubMed-3262867;
                                                                                                                                                                                                                                                                                                                                                                                       Dorow D.S., Simpson R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
1133
1026
1035
1057
1133
356
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974
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1036
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436
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TRANSMEM
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gale R.F.,
Radams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gale R.F.,
Radams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gale R.F.,
Radams M.D., Celniker S.E., Richards S., Ashburner M. Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Radandon R.C., Rogers Y.-H.C., Blazef K.G., Champe M., Pfelifer D.D.,
Radil J.F., Agbayani A., An H.-J., Andrews-Flannkoch C., Baldwin D.,
Ballew R.M., Basus A., Bacandale J., Bayraktaroglu L., Basaley E.M.,
Baltew R.M., Basus A., Bacandale J., Bayraktaroglu L., Basaley E.M.,
Baltow R.M., Basus D.A., Baraman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
Rade Pablos B., Delcher A., Deng Z., Ways A.D., Dew I., Dietz S.M.,
Cabyley S., Dahlke C., Davanes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Rade Pablos B., Delcher A., Dong Z., Ways A.D., Dew I., Dietz S.M.,
Rade Pablos B., Delcher A., Dong Z., Glann P., Harris M.L.,
Raderis J.M., Evangelista C.C., Ferraz C., Ferraz C., Ferraz C.,
Raderis D., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C.,
Jalall M., Kalush F., Karpen G.H., Ke. Z., Kenlp D., Lal Z.,
Raderis D., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C.,
Alasko P., Leil Y., Lewitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Alasko P., Leil Y., Lewitsky A.A., Li J., Li Raderson D.,
Raderis R., Mattei B., McIntoh T.C., Morris J., Woshrefl A.,
Reinert K., Remington K.A., Muxoh K., Nusskern D.R., Pacieb J.M.,
Rader E., Spradling A.C., Standers R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Standers R.D.C., Scheeler F., Shen H.,
Rader E., Shadling A.C., Standers R.D.C., Scheeler F., Shen E.,
Wallsham S.H., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
Rader S.H., Wyers E.W., Rubin G.M., Venter T.J.C.,
Radibas R.L., Robing E.W., Rubin G.M., Venter T.J.C.,
Radibas R.L., Robing E.W., Rubin G.M., Venter T.J.C.,
Radibas R.L., Rober E.W., Rubin G.M., Venter T.C.,
Radibas R.L., Rober E.W., Rubin G.M., Venter T.C.,
Radibas
                                       Kopczynski C.C., Alton A.K., Fechtel K., Kooh P.J., Muskavitch M.A.T., "Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes a protein related to blood coagulation factors and epidermal growth factor of vertebrates."; Genes Dev. 2:1723-1735(1988).
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TISSUE SPECIFICITY: DETECTED IN ALL AREAS WITH NEUROGENIC
ABILITIES, FOR EXAMPLE THE NEUROGENIC ECTODERM AND THE PRIMORDIA
OF THE SENSE ORGANS. LATER EXPRESSION IS RESTRICTED TO THOSE CELLS
THAT HAVE ADOPTED A NEURAL FATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knust E., Dietrich U., Tepass U., Bremer K.A., Weigel D., Vaessin H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.";
Development 110:905-914(1990).
-!-FUNCTION: ESSENTIAL FOR PROPER DIFFERENTIATION OF ECTODERM. DL
IS REQUIRED FOR THE CORRECT SEPARATION OF NEURAL AND EPIDEEMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campos-Ortega J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haenlin M., Kramatschek B., Campos-Ortega J.A.;
The pattern of transcription of the neurogenic gene Delta of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                melanogaster, and their relation to neurogenic genes."; EMBO J. 6:761-766(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATTERN OF TRANSCRIPTION, AND CHARACTERIZATION.
                                                                                                                                                                                                            STRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISSUE-Embryo;
MEDLINE-87218537; PubMed-3107986;
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                        MEDLINE-89196890; PubMed-3149249;
STRAIN-Oregon-R; TISSUE-Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 422-621 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome sequence of Drosc
Science 287:2185-2195(2000).
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL LINEAGES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEL.
BGF-LIKE 1.
BGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 4.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
BGF-LIKE 8.
EGF-LIKE 8.
EGF-LIKE 8.
EGF-LIKE 8.
EGF-LIKE 9.
EGF-LIKE 17.
EGF-LIKE 17.
EGF-LIKE 8.
EGF-LIKE 17.
EGF-LIKE 18.
EGF-LIKE 18.
EGF-LIKE 17.
EGF-LIKE 18.
DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY. EXPRESSION IS HIGHEST ERRLY IN EMBRYONIC DEVELOPMENT (STAGE 5) AND REDUCES TO A LOW LEVEL DURING LARVAL STAGES.

MISCELLANEOUS: SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO THE INNER PARY OF EMBRYO IS ONE OF THE FIRST STEPS OF CNS DEVELOPMENT IN INSECTS, THIS PROCESS IS UNDER CONTROL OF THE
                                                                                                                        NEUROGENIC GENES.
MISCELLANEOUS: NOTCH AND SERRATE MAY INTERACT AT THE PROTEIN
LEVEL, IT IS CONCEIVABLE THAT THE SERRATE AND DELTA PROTEINS MAY
COMPETE FOR BINDING WITH THE NOTCH PROTEIN.
SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 DSL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, X06289; CAA29617.1; --
EMBL; Y00222; CAA68369.1; --
EMBL; X003725; CAA68369.1; --
EMBL; X05140; CAA28786.1; --
PIR; S00670; S00670
PIR; A26637; A26637.
HSSP, P00740; 1EDM.
FlyBase; FBGH0000463; D1.
InterPro; IPR001635; ASX_hydroxyl.
InterPro; IPR001651; EGF-1ike.
InterPro; IPR001651; EGF-2.
InterPro; IPR001438; EGF_2.
InterPro; IPR001438; EGF_1.
InterPro; IPR001438; EGF_1.
PF6m; PF001681; EGF_5.
Pfam; PF001414; DSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO0011; EGFLAMININ.
SMART; SM00051; DSL; 1.
SMART; SM00179; EGF_CA; 4.
SMART; SM00001; EGF_Like; 5.
PROSITE; PS00010; ASX_HYDROXYL; 3.
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TRAIN—Sprague—Dawley; TISSUE—Brain;

RX MEDLINE—94216386; PubMed=7512973;

RTAIN—Sprague—Dawley; TISSUE—Brain;

RT Jaworski D.M., Kelly G.M., Hockfield S.;

RTAIN—Sprague—Dawley; TISSUE—Brain;

RT Jaworski D.M., Kelly G.M., Hockfield S.;

RT Jaworski G.M., G.M., Kelly G.M., Hockfield S.;

RT Jaworski G.M., Hockfield G., Hockfi
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Hyaluronic acid; Proteoglycan; Lectin; Signal; Sush1;
EGF-like domain; Repeat; Immunoglobulin domain; Alternative splicing;
GPI-anchor. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
BREVICAN CORE PROTEIN.
      Biochem. Biophys. Res. Commun. 216:957-963(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, X79881; CAA56255.1; --
EMBL, X86406; CAA60160.1; --
EMBL, 228366; CAA82215.1; --
EMBL, 228366; CAA82215.1; ALT_FRAME.
HSSP, P20693; 1HLJ.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000742; EGF-2.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000583; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01240; LINK; 2.
PROSITE; PS01241; LINK; 2.
PROSITE; PS00615; C_TYPE_LECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00008; EGF; 1.
Pfam; PF00047; 19; 1.
Pfam; PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodom, PD000918; Link; 2. SMART; SM0032; CCP; 1. SMART; SM00034; CLECT; 1. SMART; SM00181; EGF; 1. SMART; SM00406; IGV; 1. SMART; SM00446; LINK; 2.
                                   SEQUENCE OF 1-423 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
ProDom; PD000918; Link; 2.
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883
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        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Brevican, a chondroitin sulfate proteoglycan of rat brain, occurs as secreted and cell surface glycosylphosphatidylinositol-anchored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=96074575; PubMed=7488217;
Yamada H., Watanabe K., Shimonaka M., Yamasaki M., Yamaguchi Y.;
"cDNA cloning and the identification of an aggrecanase-like cleavage site in rat brevican.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGCB_RAT STANDARD; PRT; 883 AA. 955081, 052860; 052860; 053513; 01-0CT-1996 (Rel. 34, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 40, Last annotation update) Brevican core protein precursor (Brain enriched hyaluronan binding protein) (BEHAB protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley; TISSUE-Brain;
MEDLINE-96070828; PubMed=7592978;
Seidenbecher C.I., Richter K., Rauch U., Faessler R., Garner C.C.
Gundelfinger E.D.;
                                                                                                                                                                                                                                                                                  (POTENTIAL). (POTENTIAL).
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V -> L (IN REF. 1).

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GK -> S (IN REF. 3).

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Pred. No. 1.8;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 8.
EGF-LIKE 9.
EGF-LIKE 9.
                                                                                                                                MEDLINE-92395667; PubMed=1522591;
MEDLINE-92395667; PubMed=1522591;
Hommel U., Harvey T.S., Driscoll P.C., Campbell I.D.;
Human epidermal growth factor. High resolution solution structure and comparison with human transforming growth factor alpha.";
J. Mol. Biol. 227:271-272-27297.
I. FUNCTION: THE GROWTH FATOR STIMULATES THE GROWTH OF VARIOUS EPIDERMAL AND EPITHELIAL TISSUES IN VIVO AND IN VITRO AND OF SOME FIRBOBLASTS IN CELL CULTURE.
IL SUBCELLULAR LOCATION: Type I membrane protein.
I. SUBCELLULAR CONTAINS 9 EGF-LIKE DOMAINS.
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PROSITE; PS01186; EGF_2; 7.
PROSITE; PS01187; EGF_CA; 3.
EGF-like domain; Repeat; Growth factor; Transmembrane; Glycoprotein;
                              MEDLINE-89391964; PubMed-2789514; Furuya M., Akashi S., Hirayama K.; Thuruya M., Akashi S., Hirayama K.; The primary structure of human EGF produced by genetic engineering, studied by high-performance tandem mass spectrometry."; Biochem. Biophys. Res. Commun. 163:1100-1106(1989).
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EPIDERMAL GROWTH FACTOR.
EXTRACELLULAR (POTENTIAL).
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InterPro; IPR000561; EGF-1ike.
InterPro; IPR001346; EGF-1.
InterPro; IPR001336; EGF-1.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR000033; Idl_receptor_rep.
Pfam; PF00008; EGF; 9.
PRIMTS; PR00009; EGFCF.
SMART; SM00179; EGF_CA; 2.
SMART; SM00179; EGF_CA; 2.
SMART; SM00179; EGF_CA; 2.
SMART; SM00135; LY; 8.
PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS00010; ASX HYDROXYL; 3.
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Genew; HGNC:3229; EGF.
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MEDLINE-87066721; PubMed=3491360;
Bell G.I., Fong N.M., Stemphen M.M., Wormsted M.A., Caput D.,
Bell G.I., Tong M.S., Rall L.B., Sanchez-Pescador R.;
"Human epidermal growth hactor precursor: cDNA sequence, expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pro-epidermal growth factor precursor (EGF) [Contains: Epidermal growth factor precursor)].
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V -> L (IN REF. 2).
TV -> PA (IN REF. 2).
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SEQUENCE OF 971-1023.
MEDLINE-77117897; PubMed=300079;
Gregory H., Preston B.M.;
"The primary structure of human urogastrone.";
Int. J. Pept. Protein Res. 9:107-118(1977).
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L; Mismatches
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Nucleic Acids Res. 14:8427-8446(1986).
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Best Local Similarity 70.0.,
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883 AA;
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                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Métazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILNE-21331789; PubMed-11438922; Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.; "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-DSL signaling system during brain
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 3 precursor (Notch 3).
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21094508; Pubmed-11182080;
Tanigaki K., Nogaki F., Takahashi J., Tashiro K., Kurooka H.,
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Pred. No. 2.6;
3; Mismatches 1; Indels
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Haritunians T., Boulter J., Weinmaster G., Schanen N.C.;
"Rattus norvegious mRNA for Notch 3.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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E. J. FUNISTON: Functions as a recognite cell-face determination. Open Neutrol. 369264 and Deltal to regulate cell-face determination. Open Jugaded. 369262 and Deltal to regulate cell-face determination. Open Jugaded. 369262 and Deltal to regulate cell-face determination of properties of the cell-face determination of the cell-face determination of the cell-face determination of Son alliptones of the cell-face cell-face determination of Son alliptones. Open Jugaded. Son alliptones of the cell-face determination of Son alliptones properties of the cell-face determination of Son alliptones. Properties of the cell-face determination of Son alliptones. Open Son alliptones of the cell-face determination of Son alliptones. Open Son alliptones of the cell-face determination of Son alliptones properties properties of the cell-face determination of Son alliptones of the cell-face determination of the cell-face determination of Son alliptones of the cell-face determination of the cell-face of the cell-f
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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062059; 062058; Q9CUU0;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M).
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C-TYPE LECTIN.
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CAC Q62059;
DT 01-NOV-
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DE VETSICS
DE VETSICS
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                                                                            **Counter Control of the Paragraph and Control of two developmentally allomberg L.A. Chan W.-Y., Clerch L., Massaro D.;

**A Blomberg L.A., Chan W.-Y., Clerch L., Massaro D.;

**A Molecular cloning and characterization of two developmentally are regulated genes in rat lung.";

**Counted genes in rat lung.";

**Counted (SEP-2000) to the EmBL/GenBank/DDBJ databases.

**Connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds connecting cells with the extracellular matrix. May take part in hyaluronic acid.

**Control Control Control Secreted; extracellular matrix.**

**Control Control Control Secreted; extracellular matrix.**

**Control Control C
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                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid; Alternative splicing.
  "Proteoglycan expression in the normal rat kidney."; Nephron 77:461-470(1997).
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VERSICAN CORE PROȚEIN.
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LINK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWART; SM00034; CLECT; 1.
SWART; SM00034; CLECT; 1.
SWART; SM00181; EGF; 2.
SWART; SW001181; EGF; 2.
SWART; SW00410; EGF_CA; 2.
SWART; SW00410; EGF_CA; 2.
SWART; SW00410; EGF_CA; 2.
SWART; SW00410; EGF_CA; 1.
SWART; SW00410; EGF_CA; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
PROSITE; PS01186; EGF_CA; 1.
PROSITE; PS01186; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000142; EGF_2.
InterPro; IPR001801; EGF_Ca.
InterPro; IPR001801; EGF_Ca.
InterPro; IPR001809; Ig_like.
InterPro; IPR001804; Lectin_C.
InterPro; IPR001804; Lectin_C.
InterPro; IPR001804; Lectin_C.
InterPro; IPR001804; Link.
INTERPRO; IPR000436; Sushi_SCR_CCP.
PRINTS; PR01265; LINKMODULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF062402; AAC40166.1; -.
EMBL; U75306; AAB51125.1; -.
EMBL; AF08454; AAD46544.1; -.
EMBL; AF072892; AAC26116.1; -.
EMBL; AY007691; AAG16631.1; -.
HSSP; P01132; 1EPG.
                                                            SEQUENCE OF 2535-2738 FROM N.A.
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                       RA Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Shibata K., Konoo H., Adachi J., Fukuda S.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Gaito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Gaito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T.,

RA Garimi D., Lewis S., Matauo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schrimi L.M., Staubli E., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Carnino P., de Bonaldo M.F.,

RA Brake J., Boffelli D., Bojunga N., Carninoi P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Brownstein H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Brownstein Banotation of a full-length mouse cDNa collection.";

RA Princtional annotation of a full-length mouse cDNa collection.";

RA RILLE 4099-685-690(22001.)
                                                                             STRAIN=CS7BL/6;
MEDLINE=95181355; PubMed=7876137;
Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
"Expression of PG-M(V3), an alternatively spliced form of PG-M
without a chondroitin sulfate attachment in region in mouse and human
         Ito K., Shinomura T., Zako M., Ujita M., Kimata K.;
Multiple forms of mouse PG-M, a large chondroitin sulfate
proteoglycan generated by alternative splicing.";
J. Biol. Chem. 270:958-965(1995).
                                                                                                                                                                         SEQUENCE OF 1-1692 FROM N.A. (ISOFORM VI):
STRAIN=CS7BL/6J; TISSUE=SKin;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                        tissues.";
J. Biol. Chem. 270:3914-3918(1995).
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D32040; BAA06802.1; -
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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
MEDLINE=95122551; PubMed=7822336;
                                                                    SEQUENCE FROM N.A. (ISOFORM V3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AKO14525; BAB29411.1; -. MSPP; PO1132; 1EPG.
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GAG-BETA.
EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
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GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
DOMAIN).
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IG-LIKE V-TYPE DOMAIN.
LINK 1.
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N-LINKED (GLCNN.
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SUSHI.
                                                                                                                                                                                                                                                                                                                                             SMART; SMOOD49; EGE_CA; 1.

SMART; SMOOD09; EGE_Like; 1.

SMART; SMOO009; EGF_Like; 1.

SMART; SMOO409; IG; 1.

SMART; SMOO409; IG; 1.

PROSITE; PSOO010; ASX_HYDROXYL; 1.

PROSITE; PSO1186; EGF_2; 1.

PROSITE; PSO1187; EGF_CA; 1.

PROSITE; PSO1187; EGF_CA; 1.

PROSITE; PSO1187; EGF_CA; 1.

PROSITE; PSO1041; C_TYPE_LECTIN_1; 1.

PROSITE; PSOO41; C_TYPE_LECTIN_1; 1.
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                   InterPro; IPR001304; Lecth.C.
InterPro; IPR0001304; Lecth.C.
InterPro; IPR0001308; Link;
InterPro; IPR0000436; Sushi.SCR_CCP.
Pfam; PF000047; ig; 1.
Pfam; PF00008; BGF; 2.
Pfam; PF000084; sushi; 1.
Pfam; PF00133; X11nk; 2.
PRIWTS; PR001019; BGFBLOOD.
ProDom; PD000198; Link; 2.
SMART; SM00034; CLECT; 1.
Ig_MHC.
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Eucchinoidea; Echinacea; Echinoida; Strongylocentrotidae;
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-1- FUNCTION: FORM THE APICAL LAMINA, A COMPONENT OF THE EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: EXTRACELLULAR. IN VESICLES IN THE CYTOPLASM OF UNFERTILIZED EGGS, THEN TO THE BASE OF THE HYALIN LAYER THROUGHOUT DEVELOPMENT AND FINALLY IN THE APICAL LAMINA IN LATE EMBRYOS AND EARLY LARVAE.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; IA (SHOWN HERE) AND IB; ARE PRODUCED BY ALTERNATIVE SPLICING. THE SMALL FORM (IB) LACKS 8 EGF REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-90112459; PubMed=2514273;
Delgadillo-Fegnoso M.G., Rollo D.R., Hursh D.A., Raff R.A.;
Structural analysis of the uEGF gene in the sea urchin strongylocentrotus purpuratus reveals more similarity to vertebrate than to invertebrate genes with EGF-like repeats.";
Mol. Evol. 29:314-327(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibropellin I precursor (Epidermal growth factor-related protein 1)
                                        AND ISOFORM V3).
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Bisgrove B.W., Andrews M.E., Raff R.A.;
"Fibropellins, products of an EGF repeat-containing gene, form a
unique extracellular matrix structure that surrounds the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89196806; PubMed-2784773;
Hunt L.T., Barker W.C.;
"Avidin like domain in an epidermal growth factor homolog from a
P -> K.
MISSING (IN ISC.
MISSING (IN ISC.
A MISSING (IN ISCEOR.
26 A -> G (IN REF. 3).
348 MISSING (IN REF. 3).
I -> T (IN REF. 3).
TWHNSNS -> QFGIQTA (IN REF. 3).
"4; 071B80026BC0762D CRC64;
"5 DB 1; Length 3358;
8; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 279-476 AND 781-1064 FROM N.A. WEDLINE-87319677; Pubmed-3498216; Hursh D.A., Andrews M.E., Raff R.A.; "A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.";
                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1064 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 237:1487-1490(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FASEB J. 3:1760-1764(1989).
                                                                                                                                                                                                                                                                                                        Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                             3078 CAPGYSGDQC 3087
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                             348
1308
3052
3052
126
348
1658
                                                                                                                                                                                                                                                                                                                                                                                  CVIGYSGDXC 10
                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strongylocentrotus.
NCBL_TaxID=7668;
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                                                                        1309
349
126
348
1658
3358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989
01-FEB-1996
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P10079;
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SEQUENCE
                        VARSPLIC
VARSPLIC
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                                                                          VARSPLIC
                                                                                                     VARSPLIC
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PRESULT 15

AC P10079,
DT O1-FBR.
DT O1-FBR.
DT O1-FBR.
DT O1-FBR.
DE (UEGF.-)
GN Strong;
OC Strong
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires alreement (See http://www.isb-sib.ch/announce/or send an emmail to itenseelibrsib.ch)
DEVELOPMENTAL STAGE: MODERATE LEVELS IN UNFERTILIZED EGGS AND DURING EARLY CLEAVAGE, THEN RAPIDLY INCREASES IN ABUNDANCE BETWEEN LATE MORULA AND MESENCHYME BLASTULA STAGES TO MAXIMAL LEVELS MAINTAINED THROUGH SUBSEQUENT STAGES. EXPRESSED BOTH MATERNALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 20, CALCIUM-BINDING (POTENTIAL).
                                                                                      SIMILARITY: CONTAINS 21 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 CUB DOMAIN.
SIMILARITY: THE C-TERMINAL DOMAIN OF THIS PROTEIN IS SIMILAR
TO AVIDIN/STREPTAVIDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO0577; AVIDIN, 1.
PROSITE; PSO1180; CUB; 1.
PROSITE; PSO1186; EGF_2; 19.
PROSITE; PSO1187; EGF_CA; 18.
Biotin; Alternative spliting; EGF-like domain; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; FULL.
Biotin; Alternative spirit.
Glycoprotein; Calcium-binding,
SIGNAL 1 19 POTENTIAL.
20 1064 FIBROPELLIN I.
FROM ELIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIGHTS, PROJECT, PROJECT, PRINTS, PRODOLO; ECFBLOOD.
PRINTS, PRODOLI; ECFLAMINN.
SMART; SMO0104; CUB; 1.
SMART; SMO0109; EGE_CA; 18.
SMART; SMO0101; EGE_Like; 3.
PROSITE; PSO0010; ASX_HYDROXYL; 19.
PROSITE; PSO0577; AVIDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPORT INTERPORTS: ASX_hydroxyl.
INTERPORT IPRO000152; ASX_hydroxyl.
INTERPORT IPRO00088; Avidin.
INTERPORT IPRO00089; CUB_domain.
INTERPORT IPRO00051; EGF_11ke.
INTERPORT IPRO01081; EGF_2.
INTERPORT IPRO01881; EGF_03.
INTERPORT IPRO02049; Laminin_EGF.
Pfam; PF00008; EGF; 21.
Pfam; PF00008; EGF; 21.
Pfam; PF000431; CUB; 1.
                                                                                                                                                                                                                                                                                                                      EMBL, L08692; AAA62164.1; -.
EMBL, L08692; AAA62163.1; -.
EMBL, X17330; CAA35571.1; -.
EMBL, M17421; AA330050.1; -.
EMBL, X77533; CAA35573.1; -.
PIR; A29316; A29316.
                                                                       AND ZYGOTICALLY
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Gaps

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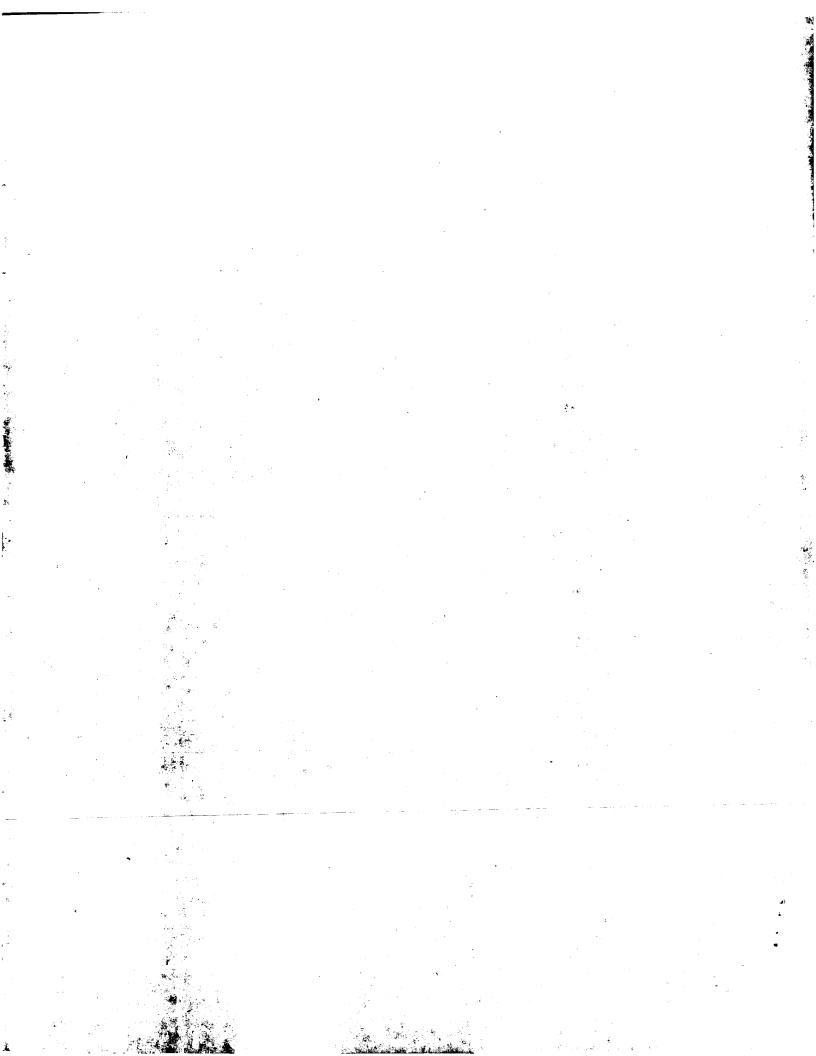
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S (IN REF. 2).
2E569CA012ED6D09 CRC64;
AVIDIN-LIKE.
BY SIMILARITY.
BY SIMIL
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60.0%;
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Best Local Similarity
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CONFLICT
SEQUENCE
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 Matches
 6; Conservative
 3; Mismatches
 1; Indels

 QY
 1 CVIGYSGDXC
 10

 Db
 316 CPLGFSGDNC
 325

Search completed: July 2, 2003, 07:31:33 Job time: 11.3333 secs



Scoring table:

Searched:

Database

Perfect score:

Title:

Run on:

Sequence:

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057409 brachydanio
057409 brachydanio
09uil7 homo sapien
042374 brachydanio
096kg6 homo sapien
09de37 brachydanio
075093 homo sapien
         028867 equus cabal
018375 drosophila
09vz44 drosophila
08t314 parameclum
019350 caenorhabdi
                                                           090xx0 orectolobus
020043 caenorhabdi
061240 halocynthia
                                                                                         bos taurus
homo sapien
dictyosteli
caenorhabdi
                                                                                                                                                                                                                                                          Q8tep7 homo sapier
Q9xuc0 caenorhabdi
Q9gsf3 podocoryne
                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-ON-2002 (TrEMBLrel. 21, Last annotation update)
Similar to epidermal growth factor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                              061240
                                                                                                Q9npk9
Q8t2m9
Q20459
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P91904
                                                                                                                                                                                                                     Q9un93
Q9un94
Q9nt67
                                                                                                                                                                                                                                                   56un60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL, BCOLT681; AAH17681.1;
R InterPro; IPR000152; ASX Lydroxyl.
R InterPro; IPR000152; ASX Lydroxyl.
R InterPro; IPR00136; EGF-1ike.
R InterPro; IPR00138; EGF-Ca.
R InterPro; IPR001031; LGL_Ceceptor_rep.
R InterPro; IPR001031; LGL_receptor_rep.
R Pfam; PR00008; EGFTG.
R PRIMTS; PR00009; EGFTGF.
R SMART; SM00119; EGFTGF.
R SMART; SM00119; EGFTGF.
R SMART; SM00119; EGFTGF.
R SMART; SM00119; EGFTGF.
R PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_3.
R PROSITE; PS01186; EGF_2; UNKNOWN_3.
R PROSITE; PS01186; EGF_2; UNKNOWN_3.
R PROSITE; PS01186; EGF_2; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNKNOWN_3.
7 MW: B6A44F7294746476 CRC64;
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088279
Q28867
018375
Q9V244
Q8T314
Q19350
Q90XXO
                                                                            061240
018977
09NPK9
08T2M9
020459
095RM9
                                                                                                                                                 09UIL7
042374
096KG6
096KG6
0509B37
075093
09GNU3
09UN93
09UN94
09UN67
09UN95
09UN95
09UN95
09UN95
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                               1515
1534
2656
3704
106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE-KIDNEY;
    Q8VD07
                                                                                                                                                                                                                                                                                                                                          RESULT 1
Q8VD07
  035452 mus musculu 054796 mus musculu 021756 caenorhabdi 081521 caenorhabdi 081522 caenorhabdi 081522 caenorhabdi 081523 caenorhabdi 099pm9 caenorhabdi 099pm9 caenorhabdi 099pm0 caenorhabdi 099pm0 caenorhabdi 099pm0 mus musculu 099r0m0 mus musculu 09wug5 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8vd07 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9vc97 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                   July 2, 2003, 07:25:01; Search time 41.3333 Seconds (without alignments) 49.850 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                             671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
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Q9VC97
Q35452
O54796
Q21756
Q8T520
Q8T520
Q8T522
Q8T522
Q8T522
Q8T522
                                                                                                                                                 BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                           sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_vertebrate:*
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sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                    sp_organelle:*
sp_phage:*
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sp_bacteria:*
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Maximum DB seq length: 200000000
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56
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Match Length DB
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                                                                                                                             1 CVIGYSGDXC 10
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homo sapien homo sapien homo sapien paracentrot caenorhabdi

homo sapten homo sapien caenorhabdi ô

Gaps

; 0

Length 1200;

DB 11;

; Score 56; DB Pred. No. 0.12; 1; Mismatches

100.0%; 90.0%; P

Conservative

Query Match Best Local Similarity Matches 9; Conserv

Q8WTP0 Q9GPN0 Q9WVB5 Q9ROM0 Q9WUG5

Result

No.

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RA MEDINE-20196006; PubMed-10731132;
RA MEDINE-20196006; PubMed-10731132;
RA Adams N.D., Celniker S.E., id P.W., Hoskins R.A., Galle R.F., Adams N.D., Celniker S.E., id P.W., Hoskins R.A., Galle R.F., Adams N.D., Channel M., Piciffer B.D., Amanatides P.G., Scherer S.E., id P.W., Hoskins R.A., Galle R.F., Sutton G.G., Worthan J. R., Yandell M.D., Zhang O., Chan L.X., An Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., R. Abril J.F., Agbayani A., Baxandala J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basul A., Baxandala J., Bayraktaroglu L., Beasley E.M., Ballew R., Bauthan M., Bouck J., Broketeln P., Brottler P., R. Ballew R., Doyle C., Baxter E.G., Helf G., Nelson C., Berdstein P., Brottler P., R. Benson R.Y., Dence P.V., Berman B.P., Bhandari D., Botchian D., Botchian M.R., Bouck J., Broketeln P., Brottler P., Garler E., Caher A., Chandra I., R. Beblos B., Deliber A., Dank S.D., Dew I., Datez S.M., Duckon K., Dowy D.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunkov B.C., Gabriellan A.E., Garg V.S., Gelbart W.M., Gong E., Mays A.D., Dew I., Dietz S.M., Robert G., Gabriellan A.E., Garg V.S., Gelbart W.M., Gong E., Mays A.D., Dew I., Degaser K., Jalail M., Kalush F., Karpen G., Rez., Kennisson J., R. Alaris M.L., Harvey D., Henman T.J., Well M.-H., Ibegwan C., Jalash M.-K., Martis M., Howland T.J., Well M.-H., Ibegwan C., Jalail M., Alattel B., Kodire G.H., Kez'z. Kennisson J., Moshrefi A., Mount S.M., Murphy B.L., Murphy D.M., Mushen D.L., Mount S.M., Muy M., Murphy B.M., Musher B.C., Siden K., May M., Murphy B.M., Musher B.C., Scheeler F., Spradling A.C., Stapleton M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M. Reinert K., Remington K., Saunders R.D., Scheeler F., Spradling A.C., Stapleton M., Strops M., Strops M., Strops M., Strops M., Shirk R.F., Spradling A.C., Stapleton M., Strops W., Zhang S., Zhan M., Venner E., Wang Z., Shen H., Shong F.M., Rhong F.M., Rhong
                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                PRT; 2146 AA
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; laminin_G; 3.
                                   992 CVIGYSGDRC 1001
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1 CVIGYSGDXC 10
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OR CG6383.
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PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00011; EGFLAMININ.
SMART; SM00109; EGF_CA; 11.
SMART; SM00109; EGF_CA; 11.
SMART; SM00282; LamG; 3.
PROSITE; PS00010; ASX_HYDROXYL; i6.
PROSITE; PS01186; EGF_2; 1; 25.
PROSITE; PS01186; EGF_2; 1; 7.
PROSITE; PS01187; EGF_CA; 13.
Calcium-binding; EGF_1ike domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 2146 AA; 233570 WW; 8E23B9E32B761115 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
ROWEN L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.;
Sequence of the mouse major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                              Score 51; DB 5; Length 2146;
Pred. No. 1.8;
2; Mismatches 1; Indels
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EGF-like domain; Glycoprotein.
SEQUENCE 4006 AA; 435471 MW; 553FBE873498A4FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
BMBL; AF030001; AAB82015.1; -
HSSP; PO2671; IP2D.
InterPro; IPR005561; EGF-11ke.
InterPro; IPR005561; Fubrinogen_C.
InterPro; IPR003861; Fn_III.
Pfam; PF00008; EGF; 15.
Pfam; PF000147; fibrinogen_C; 1.
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Last annotation update)
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PROSITE; PS00022; EGF_1; UNKNOWN_19.
PROSITE; PS01186; EGF_2; 19.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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70.0%;
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SMART; SW00011: EGF_11ke; 2.
SMART; SW00186; FBG, 1.
SMART; SW00060; FN3; 24.
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Best Local Similarity 70.00,
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Best Local Similarity 70.0
Matches 7; Conservative
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532 CAVGYSGDDC 541
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054796
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Gaps
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Caenorhabditis briggsae.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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Caenorhabditis briggsae.
Eukaryota: Metazoa: Nematoda: Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-PBB00;
Graudstein A., Gaspar J.M., Walters J.R., Palopoli M.F.;
"Levels of DNA polymorphism vary with mating system in the nematode
genus Caenorhabditis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.5%; Score 49; DB 5; Length 372; 70.0%; Pred. No. 0.67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                              "The sequence of C. elegans cosmid R05G6.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8T5Z1;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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2; Mismatches
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EMBL; AF491462; AAM09702.1;
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Best Local Similarity 70.v.
70.v.
Conservative
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Matches 7; Conservative
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233 CYLGYSGDKC 242
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53 CPLGYSGDYC 62
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191 AA;
                             STRAIN-BRISTOL N2;
Murray J., Le T.T.;
"The sequence of C.
                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Waterston R.;
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  SEQUENCE FROM N.A.
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SEQUENCE
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Q8T521
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STRAIN-FI BETWEEN C57BL6, AND CBA;
MEDLINE-94216385; PubMed-7512972;
Matsumoto K., Saga Y., Ikemura T., Sakakura T., Chiquet-Ehrismann R.;
The Distribution of tenascin-X is distinct and often reciprocal to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIRW-II BETWEEN STRIG.
MEDIJINE-99014231; PubMed-9795100;
Ikuta T., Sogawa N., Ariga H., Ikemura T., Matsumoto K.;
Structural analysis of mouse tenascin-X: evolutionary aspects of reduplication of FNIII repeats in the tenascin gene family.";
Gene 217:1-13(1998).
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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PROSITE; PROD022; EGF_1; UNKNOWN_19.
PROSITE; PS01186; EGF_2; 17.
PROSITE; PS0514; FIBRIN AG_C_DOMAIN; 1.
EGF-like domain; Glycoprotein
SEQUENCE 4114 Aa; 447268 MW; 45FE7AD5145881Al CRC64;
01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 39.1 kDa protein.
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InterPro; IPR000561; EGF-like.
InterPro; IPR002181; Fibrinogen_C.
InterPro; IPR003961; FN_III.
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STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
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J. Cell Biol. 125:483-493(1994).
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Pfam; PF00147; fibrinogen_C; 1.
Pfam; PF00041; fn3; 31.
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SMART; SM00001; EGF_11ke; 2.
SMART; SM00186; FBG; 1.
SMART; SM00060; FN3; 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :|||||:|
CAVGYSGDDC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CVIGYSGDXC 10
                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 7; Conserv
                                                                                                                                                                                NCBI_TaxID=10090;
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                                                      Penascin-X.
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021756;
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Matches
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6238;
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Graustein A., Gaspar J.M., Walters J.R., Palopoll M.F.;
"Levels of DNA Polymorphism vary with mating system in the nematode genus Caenorhabditis.";
Genetics 0:0-0(2002).
EMBL: AR491458; AAM09698.1; -.
NON_TER 194 194
SEQUENCE 194 AA; 21275 MW; 07313C8ABD9C65C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6238;
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MDDLINE-21100341; PubMed-11156985;
Rudel D., Kimble J., Stanle J
                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 70.0%; Pred. No. 0.52;
Matches 7; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JON-2002 (TrEMBLrel. 21, Last annotation update)
Notch-like transmembrane receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 5;
Pred. No. 0.52;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             963 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                      Genetics 0:0-0(2002).
EMBL; AF491459; AAM09699.1; -.
EMBL; AF491461; AAM09701.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.7%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                     genus Caenorhabditis.";
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Matches 7; Conservative
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Caenorhabditis briggsae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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56 CPLGYSGDYC 65
                                                                                                                                                                                                                                                                                                                                                            1 CVIGYSGDXC 10
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56 CPLGYSGDYC 65
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SEQUENCE FROM N.A.
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Q8T5Z3;
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                                                                                                                              Graustein A., Gaspar J.M., Walters J.R., Palopoli M.F.; "Levels of DNA polymorphism vary with mating system in the nematode genus Caenorhabditis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glp-1 (Fragment).
Caenorhabditis briggsae.
Caenorhabditis briggsae.
Ebkaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Graustein A., Gaspar J.M., Walters J.R., Palopoli M.F.;
Graustein A., Gaspar J.M., Walters J.R., Palopoli M.F.;
Graustein A., Gaspar J.M., Walters J.R., Palopoli M.F.;
genus Caenorhabditis.";
Genetics 0:0-0(2002).
Genetics 0:0-0(2002).
NON_TER 193 A.M. 193
SEQUENCE 193 AA; 21178 MW; 42135BBBEBBE02C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Caenorhabditis briggsae.
Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae; Rhabditidae; Reconstrated Caenorhabditis.
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SEQUENCE FROM N.A.
STRAIN-HK104, AND HK105;
Graustein A., Gaspar J.M., Walters J.R., Palopoli M.F.;
"Levels of DNA polymorphism vary with mating system in the nematode
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                                                                                                                                                                                                                                                                                                                                                                                   85.7%; Score 48; DB 5; Length 191; 70.0%; Pred. No. 0.52; rative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.7%; Score 48; DB 5; Length 193; 70.0%; Pred. No. 0.52; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                  191 191
191 AA; 20943 MW; 2EEB21B5F47FB470 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                            Genetics 0:0-0(2002).
EMBL; AF491463; AAM09703.1; -.
NON_TER 191 191
SEQUENCE 191 AA; 20943 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Matches 7; Conservative
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53 CPLGYSGDYC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CVIGYSGDXC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CVIGYSGDXC 10
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55 CPLGYSGDYC 64
                                                                             SEQUENCE FROM N.A.
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                            NCBI_TaxID=6238;
                                                                                                          STRAIN-VT847;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Q8T5Z2;
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Q8STG0;
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081522
10 081523
DT 01-JT
DT 01-JT
DT 01-JT
DE 0
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650 CHVGYSGDHC 659
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                                                                                                                           RESULT 13
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                                                                                                                                                       09GPN0
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Sawada H., Sakai N., Abe Y., Tanaka E., Takahashi Y., Fujino J.,
Sawada H., Sakai N., Abe Y., Tanaka E., Takahashi Y., Fujino J.,
Kodama E., Takizawa S., Yokosawa H.,
Nodama E., Takizawa S., Yokosawa H.,
A Novel Sperm Receptor VC70, Consisting of 12 EGF-like Repeats, Is
Degraded by the Ubiquitin-Proteasome Pathway during Ascidian
Ferfilization.",
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ABG61740; BAB72021.1;
InterPro; IPR0006152; Asx_hydroxyl.
InterPro; IPR0006152; Asx_hydroxyl.
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Pred. No. 3.3;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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PROSITE; PS00022; EGF_1; UNKNOWN_13.
PROSITE; PS0186; EGF_2; UNKNOWN_10.
SEQUENCE 1162 AA; 124499 MW; 26F57DE32B1A8E6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 963 AA; 106394 MW; 52BF80010E12FB57 CRC64;
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Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                         SMART; SM00248; ANK; 5.

R SMART; SM00181; EGF; 5.

R SMART; SM00101; EGF, 1.

R SMART; SM00001; EGF_11ke; 4.

SMART; SM00001; EGF_11ke; 4.

R PROSITE; PS50297; ANK REDEAT; 3.

PROSITE; PS50297; ANK REDEAT; 3.

PROSITE; PS0010; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01186; EGF_1; UNKNOWN_4.

ANK REPEAT; 1.

ANK REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.7%; Score 48; DB 5; 70.0%; Pred. No. 2.7; rative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000742; EGF_2.
Interpro; IPR001438; EGF_1I.
Interpro; IPR001438; EGF_II.
Interpro; IPR001507; Endoglin/CD105.
Pfam; PF00008; EGF; 13.
PRIMTS; PR00010; EGFBLCOD.
SMART; SM00181; EGF; 14.
SMART; SM00241; ZP; 1.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
                                                     InterPro; IPR000742; EGF_2.
InterPro; IPR002049; Laminin_EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vitelline coat component HrVC120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halocynthia roretzi (Sea squirt).
                                                                                                           InterPro; IPR000000; Nutch. Pfam; PF00023; ank; 6. Pfam; PF00008; EGF; 4. Pfam; PF00006; notch; 3. PRINTS; PR00011; EGFLAMININ. PRINTS; PR01452; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.7%;
70.0%;
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Best Local Similarity 70.0.
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Best Local Similarity 70.0.
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123 CPLGYSGDYC 132
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SO PR PROPERTY SO 
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1 CVIGYSGDXC 10

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                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                               Rudel D., Kimble J.; "Conservation of glp-1 regulation and function in nematodes."; Genetics 157:639-654(2001). "EMBL; AF315554; AAG49316.1; -- HSSP; PO1132; 1EGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1270 AA; 138964 MW; A7662EB575A4B61B CRC64;
                                           01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.7%; Score 48; DB 5; 70.0%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANK repeat; Receptor; Repeat; Transmembrane
SEQUENCE 1270 AA; 138964 MW; A7662EB5755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWART; SW00248; ANK; 5.
SWART; SW00181; EGF; 12.
SWART; SW00109; EGF_CA; 10.
SWART; SW00001; EGF_LIKe; 8.
SWART; SW00004; NL; 3.
PROSITE; PS50088; ANK_REPEAT; 3.
PROSITE; PS50297; ANK_REP_REGION; PROSITE; PS00100; ASX_HYDROXYL; 2.
PROSITE; PS01186; EGF_2; 8.
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPR002110; ANK.
InterPro: IPR001513; Asx_hydroxyl.
InterPro: IPR000051; EGF-1ike.
InterPro: IPR000142; EGF-2.
InterPro: IPR001881; EGF-Ca.
InterPro: IPR002049; Laminin_EGF.
InterPro: IPR000800; Notch.
Pfam; PF00003; ank; 6.
Pfam; PF00008; EGF; 10.
                                                                                                                                                                                                                                                                                                      STRAIN-AF16;
MEDLINE-21100341; PubMed-11156985;
                                                                                                                 Notch-like transmembrane receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00066; notch; 3.
PRINTS; PR00011; EGFLAMININ.
PRINTS; PR01452; NOTCH.
PRELIMINARY;
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hes 7; Conservative
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                                                                                                                                                        Caenorhabditis briggsae
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Search completed: July 2, 2003, 07:28:38
Job time: 42.3333 secs
            MEDLINE-99418630; PubMed-10490098;
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Best Local Similarity 70.0
Matches 7; Conservative
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                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-99365246; PubMed-10433822;
Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.W.;
"The mouse SLIT family: secreted ligands for ROBO expressed in patterns that suggest a role in morphogenesis and axon guidance.";
EMBL; AF144627; AAD44758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 4.4;
4; Mismatches 0; Indels
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PROSITE: PSO1185; CTCK_1; UNKNOWN_1.
PROSITE: PSO1225; CTCK_2; 1.
PROSITE: PSO1022; EGF_1: UNKNOWN_9.
PROSITE: PSO1186; EGF_2; 8.
PROSITE: PSO1187; EGF_0A; 2.
Calcium-binding: EGF_1ike domain; Glycoprotein; Repeat.
SEQUENCE 1531 AA; 167546 WW; F7D09AA6693A4F30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Last sequence update)
Last annotation update)
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                                                                                                          MGD; MGI:1115203; Slit1.
InterPro; IPR000152; Ast_hydroxyl.
InterPro; IPR000159; Cys_knot.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Z.
InterPro; IPR001881; EGF_Z.
InterPro; IPR001438; EGF_I.
InterPro; IPR001438; EGF_I.
InterPro; IPR001438; EGF_I.
InterPro; IPR00151; Laminin_G.
                                                                                                                                                                                                            IPR001611; LRR.
IPR000483; LRR_Cterm.
IPR000372; LRR_Nterm.
                                                                                                                                                                                                                                                         Pfam; PF00008; EGF; 9.
Pfam; PF00054; laminin_G; 1.
Pfam; PF00560; LRR; 19.
Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRUT; 4.
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                       LRR_typ.
                                                                                                                                                                                                                                           IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                          CT; 1.
EGF_CA; 2.
EGF_like; 7.
FOLN; 2.
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                                                                                                                                                                                                                                                                                                                                                               SWART; SM00282; Lami; 1.
SWART; SM00370; LRR; 3.
SWART; SM00082; LRRCT; 4.
SWART; SM00013; LRRCT; 4.
SWART; SM00013; LRRUT; 4.
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InterPro; IPR001611;
InterPro; IPR000483;
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Matches 6: Conserve
  NCBI_TaxID=10090;
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SMART; SM00274;
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Q9R0M0;
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AA USULIANE-1994180518, FUDMEGG=104940198;

RA USULIANE-1994180518, FUDMEGG=104940198;

RA Taketchi M., UGMURTA T.;

Flankingo, a seven-pass transmembrane cadherin, regulates planar cell

RI Plankingo, a seven-pass transmembrane cadherin, regulates planar cell

RI Cell 98:585-595(1999).

C -1 SIMILANITY: CONTAINS 9 CADHERIN DOMAINS.

DR MEDL; ABO28499; BAA844070.1; —

EMBL; ABO28499; BAA844070.1; —

R MSSP; PO0740; IEDM.

DR MISSP; PO0740; IEDM.

DR MISSP; PO0740; IEDM.

DR InterPro; IPR000126; Cadherin.

DR InterPro; IPR000126; Cadherin.

DR InterPro; IPR000180; Dormm_receptor.

DR InterPro; IPR000180; Dormm_receptor.

DR InterPro; IPR00199; Laminin_GF.

DR InterPro; IPR001030; PRD_Cys_rich.

DR InterPro; IPR001030; PRD_Cys_rich.

DR InterPro; IPR001030; PRD_Cys_rich.

DR InterPro; IPR001030; PRD_Cys_rich.

DR Ffam; PP001030; Trm_2; 1.

DR Pfam; PP00002; Cadherin; 9.

DR Pfam; PP00002; Cadherin; 9.

DR Pfam; PP00002; Cadherin; 9.

DR Pfam; PP00004; GGF; 5.

DR Pfam; PP00004; GGF; 5.

DR Pfam; PP00005; Cadherin.

DR Pfam; PP00019; GGFCECRETIN.

DR PRINTS; PR002015; GPSLMININ.

DR PRINTS; PR002015; CADHERIN.

DR PRINTS; PR002015; CADHERIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50268; CADHERIN_2; J.
PROSITE; PS50022; EGF_1; UNKNOWN_6.
PROSITE; PS00186; EGF_2; 2.
PROSITE; PS5027; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50361; G_PROTEIN_RECEP_F2_4; 1.
PROSITE; PS01248; LAMININ_IYPE_EGF; UNKNOWN_1.
Calclum-binding; Cell adhesion; EGF-like domain; Glycoprotein.
SEOUENCE 2920 AA; 317648 MW; 2919558DF467114F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 8.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS00232; CADHERIN_1; 5.
PROSITE; PS50268; CADHERIN_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PRO0249; GPCRSECRETIN. SMART; SM00112; Ca; 9. SMART; SM00101, EGF_Lam; 1. SMART; SM00001, EGF_Like; 6. SMART; SM00008; HOTMR; 1. SMART; SM00282; LamG; 2. SMART; SM00282; LamG; 2. SMART; SM00208; TNFR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.78;
70.08;
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2, 2003, 07:25:01 ; Search time 43.3333 Seconds
(without alignments)
30.750 Million cell updates/sec
                                                                                                                                                                                                                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                   908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                             1 CVIGXSGDXC 10
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Chimeric epidermal Mouse NRG-2 EGF-1i N terminal of rat Rat epithelial gro Rat epidermal grow Rat epidermal grow Human Neuregulin-2

Human transmembran Herbicidally activ Rat cerebellum der

Human novel polype

ALIGNMENTS

Human transmembran

AAB3519(

Angiotensin conver Mouse epidermal gr Drosophila melanog Human versican iso Human cancer assoc Human MOLIb protei

Angiotensin conver Angiotensin conver Angiotensin conver

Angiotensin conver Recombinant human Angiotensin conven

conver

Mouse epidermal gr Modified mouse epi Epidermal growth f

AAU76704 AAU76706 AAP60791

Versican. Homo sa Human MOLla protei Human Notch2 (humN Zebrafish Delta-B

AAE18208 AAR12609 AAY06816

1473 2409 2469 2471

1073 1080 2146

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT

/SIDS2/gcgdata/geneseq/genesegp-emb1/AA1998 /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1999

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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.

.DAT:*

Nelson J, Walker B, McFerran N, Harriott P;

(UYBE-) UNIV QUEENS BELFAST.

XX AX I

RESU	RESULT 1	
AAX	AAY52143	
£	AAY52143 stand	AAY52143 standard; peptide; 10 AA
×		
AC	AAY52143;	
XX		
Ω	28-JAN-2000 (first entry)	first entry)
XX	•	
DE	Mouse EGF deri	Mouse EGF derived peptide for targetting laminin receptor.
×		
ΚW	Epidermal grow	Epidermal growth factor; EGF; laminin receptor; anglogenesis;
ΧX	medicament; wo	und healing; retinopathy of immaturity; metastatic cancer
ΚW	candida infect	candida infection; leishmania; trichomonas vaginalis.
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os	Mus sp.	
×		
FH	Key	Location/Qualifiers
FT	Modified-site	·
FT		/note= "Acetyl-Cys (S-ACM)"
FT	Modified-site	10
FT		/note= "Cys (S-Acm)-NH2"
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PN	W09954356-A1.	
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PD	28-OCT-1999.	
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PF	21-APR-1999;	99WO-GB01211.
×		
PR	22-APR-1998;	98GB-0008407.

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                                                                                                                                                                                                                                                                                                                                                                                                 This is a peptide derived from mouse epidermal growth factor (EGF) residues 33-42. This peptide is used in the invention to prepare a composition to target laminin receptors. EGF derived peptides inhibit blood vessel formation through their antagonism of the high affinity 67kD laminin receptor found on endothelial cells. The peptide is modified in the preparation of a medicament for binding to laminin receptors as an (ant) agonist. The medicament is also useful for healing endothelial cell wounds and treating anglogenic diseases, especially rethopathy of finantial concert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel.ErbB-4 ligand, neuregulin-4 (NRG-4). NRG-4 binds to mammalian ErbB-4 receptor and can be expressed by standard recomplinant methodology. Pharmaceutical compositions comprising NRG-4 are
                                                                                                                                                                                        Candida spp. infection, and parasitic infestations like leishmania and trichhomonas vaginalis. The peptide are anti-anglogenic in human models. The peptides also inhibit both laminin- and EGF-stimulated angiogenesis, and prevent tumour cell attachment to basement membranes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel ErbB-4 ligand, referred as neuregulin (NRG)-4 and polynucleotide sequences encoding NRG-4, useful. for upregulating or downregulating ErbB-4 receptor activity to treat Alzheimer's disease, stroke, gastric
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ErbB-4; neuregulin-4; NRG-4; pro-NRG-4; neuroprotective; vulnerary;
cerebroprotective; vasotropic; antiparkinsonian; anticonvulsant;
cytostatic; nootropic; EGF; NRG-2.
                                                                                                                                                                                                                                                                                              ö
                                New peptide derived from murine epidermal growth factor (mEGF)
                                                                                                                                                                                                                                                                       ; DB 21; Length 10; 0.51;
                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                 Pred. No. 0.51
2; Mismatches
                                                                                                                                                                                                                                                                       Score 50;
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                                                                                                                                                                                                                                                                                                                                                                                            AAG66047 standard; peptide; 47 AA.
                                                     Claim 4; Page 28; 35pp; English
                                                                                                                                                                                                                                                                    100.0%;
80.0%; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                              Similarity 80.08; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse EGF motif sequence.
                                                                                                                                                                                                                                                                                                                  1 CVIGXSGDXC 10
                                                                                                                                                                                                                                                                                                                             1 CVIGYSGDRC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yarden Y;
          WPI; 2000-013229/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-041398/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200181540-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harari D,
                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                   AAG66047;
                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
AAG66047
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useful for regulating an endogenous protein affecting ErbB-4 receptor activity in vivo. They are also useful for treating or preventing a disease condition or syndrome associated with disregulation of an endogenous protein affecting ErbB-4 receptor activity, e.g., amyotrophic atcepts protein affecting ErbB-4 receptor activity, e.g., amyotrophic atrophy, brain trauma, stroke, ischemia, Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's concer, cervical carcinoma, endometrial adenocarcinoma, pancreatic prostate, breast and ovarian cancer, cervical carcinoma, endometrial adenocarcinoma, pancreatic D cells-somatostatinoma and Zollinger-Ellison syndrome. The agent comprised in the pharmaceutical composition includes a polypeptide (e.g., a soluble lighand binding domain of ErbB-4 i.e., IgB4; or a monoclonal, polyclonal, humanized, single chain antibody or an immunoreactive derivative of an activity. Traceable synthetic/recombinant NRG-4-tagged molecules can serve as a diagnostic tool in which cells binding NRG-4 can be measured, Sequences AAGG66044-53 represent the EGF-like motifs of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthesis of epidermal growth factor polypeptide - by condensation of protected smaller peptide sequences, de:protection then oxidn. to cyclise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The amino acid sequence is that of an epidermal growth factor tripentacontapeptide which is synthesised by condensation of protected smaller peptide sequences. This method produces the peptide smoothly, with high purity and yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epidermal growth factor tripentacontapeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB Pred. No. 2; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP40315 standard; protein; 53 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | | | : | | | : | | 33 CVIGYSGDRC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CVIGXSGDXC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1984-072465/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth factors.
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Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP59027858-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-AUG-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-FEB-1984.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP40315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
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Cell growth factor; viscoelastic solution; fibroblastic growth factor; FGF; epidermal growth factor; EGF; buffered solution; lubrication; carboxypropyl methylcellulose; cellulose gum; dextran; dextran sulphate; chondroitin sulphate; sodium hyaluronate; osmolarity; mitogenic; wound healing; cell protection; cell coating; surgery; tissue space; hydroxypropyl methylcellulose; manipulation.
                                                                                                                                                                                                                                                                                                                                                    The human rEGF is used to treat oversecretion of gastric acid or epithelial wound. EGF is modified to increase its chemical stability. Its storage life is improved without diminishing its biological activity. The proteins may be prepared by traditional chemical or recombinant means.
                                                                                                                                                                                                                                                                                      Human epidermal growth factor – is substituted at position 11 greater stability and improved storage life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Given in the specification as Try"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; DB 11;
Pred. No. 2.3;
2; Mismatches 0;
  epithelial wounds; gastric acid secrection.
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Misc-difference 11..11
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                                                                                                                                                                                                                                                                                                                               Claim 9; Page 25; 32pp; English.
                                                                                                                                                                                                                               Medina-Selby A;
                                               11..11
/label= E, N,
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80.0%;
                                                                                                                                                                        89US-0351773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic human/mouse EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                          WPI; 1990-361427/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CVIGXSGDXC
                                                                                                                                                                                                    CHIR-) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 AA;
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Misc-difference
                                                                                                                                                                                                                               Nascimento CG,
                                                                                                                                                                       12-MAY-1989;
                                                                                                                                            09-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1988;
                                                                                    WO9013570-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5366964-A.
                                                                                                                15-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR67275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The inventors claim synthetic peptides which correspond to sequences occurring in EGF, but excluding EGF. The synthetic peptides correspond to active sequences from EGF fragments: 3-14, 12-14, 12-15, 3-10, 29-37 and 33-37 (Claims 2-7 and AAP91659-P91664 resp.). The peptides are analogenic. Their relative shortness means that they pose fewer synthesis problems than the entire EGF molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                         Gaps
                                                                                                                                                                                                                                                                      Amino acid sequence for naturally occurring epidermal growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stimulating angiogenesis \dot{} to amino acid sequences occuring in
                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified murine epidermal growth factor; stability; storage;
                            Length 53;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                 Epidermal growth factor; angiogenesis; synthetic peptide
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 50; DB 10;
80.0%; Pred. No. 2.3;
ive 2; Mismatches 0;
                            Score 50; DB 5;
Pred. No. 2.3;
2; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified murine epidermal growth factor.
                                                                                                                                                                                    AAP91658 standard; protein; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR08007 standard; protein; 53 AA
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                            100.0%;
80.0%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic peptide active in has sequences corresponding epidermal growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                 87AU-0003629
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                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 1; 1/1; 11pp; English
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                                                        Conservative
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33 CVIGYSGDRC 42
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                                                                                    1 CVIGXSGDXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1989-068852/09
                                       Similarity
8; Conserv
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Best Local Similarity
53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                10-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                         23-FEB-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McAuslan BR;
                                                                                                                                                                                                                                          29-JUN-1990
                                                                                                                                                                                                                                                                                                                                             WO8901489-A
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                         Query Match
Best Local S
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 Sequence
                                                                                                                                                                                                                AAP91658;
                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR08007
ID AARC
XX
AC AARC
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DT 25-F
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Indels

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Length 53;

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This is a chimeric epidermal growth factor (EGF) protein AC. This chimeric EGF protein contains sequences derived from human and mouse EGF sequences. The chimeric EGF proteins can be recombinantly produced by culturing a microorganism of the genus Bacillus transformed by an expression vector containing the encoding DNA molecules. The recombinant chimeric EGF proteins exhibit a wide variety of physiological activities similar to those of naturally occurring EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                         Chimeric epidermal growth factor proteins - and DNA molecules for their recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Epidermal growth factor; EGF; chimeric; human; mouse; recombinant.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 50; DB 18; Length 53; 80.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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48.53
/note= "region D from human EGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "region A from mouse EGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric epidermal growth factor protein ABC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "region B from mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW34467 standard; Protein; 53 AA.
                                                                                                                                                                                                       Claim 5; Page 26; 40pp; English.
             96JP-0123970.
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.00,
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                                          (HGET ) HIGETA SHOYU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Mus sp.
- Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HGET ) HIGETA SHOYU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 CVIGYSGDRC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVIGXSGDXC 10
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/note=
                                                                            Tanaka A;
                                                                                                       WPI; 1997-550187/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tagami H, Tanaka A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-550187/51.
N-PSDB; AAT99942.
                                                                                                                                                                                                                                                                                                                                                                       53 AA;
                                                                                                                          N-PSDB; AAT99941
           23-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU9717759-A.
                                                                           Tagami H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW34467;
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                      The sequences given in AAR67273-76 are cell growth factors which may be used in the viscoelastic solution of the invention. The peptides are defived from fibroblastic growth factor (FGF) and epidermal growth factor (FGF). The viscoelastic solution also comprises a growth factor (FGF). The viscoelastic solution also comprises a buffered solution which is pref. a buffered balanced salt solution, at least 1 of hydroxy- or carboxypropyl methylcellulose, a cellulose gum, dextran or dextran sulphate, chondroith sulphate, and sodium hyaluronate. It has a pH of 6-8 and an osmolarity of 200-400 moSmol/1. The growth factors are mitogenic in vitro for a wide range of tissues and the viscoelastic soln. may be used as a surgical soln. which is in direct contact with cells undergoing wound healing. It also provides a cell protection and cell coating during surgery. The soln. provides maintenance of tissue space, hydroxypropyl methylcellulose and now hall contact with the tissue, while sodium hyaluronate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                           Viscoelastic soln. contg. hydroxypropyl methylcellulose, sodium hyaluronate, chondroitin sulphate and growth factors - used as a surgical soln. to promote wound healing, e.g. of corneal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Epidermal growth factor; EGF; chimeric; human; mouse; recombinant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 50; DB 16; Length 53; 80.0%; Pred. No. 2.3; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "region A from mouse EGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "region D from human EGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric epidermal growth factor protein AC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "region C from mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "region B from
                                                                                                                                                                                                          Disclosure; Column 5; 8pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW34466 standard; Protein; 53 AA.
89US-0434305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       provides tissue manipulation
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- Homo sapiens.
                                                                              Lindstrom RL, Skelnik
                              LINDSTROM R L.
SKELNIK D.
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48..53
/note=
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                                                                                                             WPI; 1995-005865/01.
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CVIGYSGDRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 AA;
13-NOV-1989;
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Chimeric
                                              (SKEL/)
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                              (LIND/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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AAW34466 RESULT 7

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centrifugation or membrane filtration.
                                        Sednence
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                                                                                                                                                                                                                                                                                  ö
                                                                                  This is a chimeric epidermal growth factor (EGF) protein ABC. This chimeric EGF protein contains sequences derived from human and mouse EGF sequences. The chimeric EGF proteins can be recombinantly produced by culturing a microorganism of the genus Bacillus transformed by expression vector containing the encoding DNA molecules. The recombinant chimeric EGF proteins exhibit a wide variety of physiological activities similar to those of naturally occurring EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents mouse epidermal growth factor (EGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolation of recombinant epidermal growth factor from whole broth by fluidised-bed ion-exchange chromatography
          Chimeric epidermal growth factor proteins - and DNA molecules for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; epidermal growth factor; EGF; isolation; recombinant;
                                                                                                                                                                                                                                                     DB 18; Length 53;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ion exchange chromatography; Bacillus brevis
                                                                                                                                                                                                                                                       100.0%; Score 50; DB 80.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                        Pred. No. 2.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW50134 standard; protein; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Warren B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 26; 38pp; English.
                                                              Claim 6; Page 26; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse epidermal growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97AU-0028698.
                                their recombinant production
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                       1 CVIGXSGDXC 10
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33 CVIGYSGDRC 42
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                                                                                                                                                                                                                             53 AA;
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The present sequence represents a protein which has epidermal growth factor (EGF) like activity, from the present invention. The present invention describes a method for the isolation of recombinant epidermal growth factor (EGF) from whole broth. The method comprises: (a) passing a culture containing the protein upwards through a column containing a culture containing the protein upwards through a column containing a disorbed metraial, allowing the ion exchanger to remove non-adsorbed meterial, allowing the ion exchanger to settle, and eluting adsorbed protein by passing an eluant downwards through the column; (b) adsorbed protein by passing an eluant downwards through the column; (b) filtering the eluate through a membrane with a molecular weight cutoff of $5000. The method is for isolating recombinant molecular weight cutoff of $5000. The method is for isolating recombinant human, mouse, pig or rat EGF, or an EGF analogue with one of four human, mouse, pig or rat EGF, or an EGF analogue with one of four human, mouse, pig or rat EGF, or an EGF analogue with one of four human, mouse, pig or rat EGF, or an EGF analogue with one of four human, muster, the EGF proteins can be recovered in high yield and brevis cultures. The EGF proteins can be recovered in high yield and high purity without the need to pretreat the culture broth to remove the calls, e.g. by costly centrifugation or membrane filtration.
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                                                                     Gaps
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                  Length 53;
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80.0%; Pred. No. 2.3;
iive 2; Mismatches 0;
                                                                           ö
                  DB 19;
Pred. No. 2.3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epidermal growth factor analogue 3.
                                                                                                                                                                                                                                                                                                                                       AAW50139 standard; protein; 53 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 28; 38pp; English.
                           100.08;
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                                                      80.08;
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                                                                              Conservative
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Best Local Similarity
      Query Match
Best Local Similarity
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Merozoite surface protein; protazoacide; vaccine; malaria; human; EGF; epidermal growth factor.
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CVIGYSGDRC 42
                                                                                                                                                                                                                                                                            WPI; 2001-015762/02.
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Best Local Similarity
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                                                                               WO200063245-A2.
                                                      Homo sapiens.
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                                                                                                                                                                                           25-MAY-1999;
                                                                                                                                                                 20-APR-1999;
                                                                                                            26-OCT-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a protein which has epidermal growth factor (BGF) like activity, from the present invention. The present invention describes a method for the isolation of recombinant epidermal growth factor (BGF) from whole broth. The method comprises: (a) passing fluidised bed of ion exchanger, washing the ion exchanger to remove non-scanned material, allowing the ion exchanger to settle, and eluting a disorbed material, allowing the ion exchanger to remove non-gasorbed protein by passing an eluant downwards through the column; (b) filtering the eluter through a membrane with a molecular weight cutoff of 5000. The method is for isolating recombinant column, mouse, pig or rat EGF, or an EGF analogue with one of four human, mouses, pig or rat EGF, or an EGF analogue with one of four cheris cultures. The EGF proteins can be recovered in high yield and thish purity without the need to pretreat the culture broth to remove the colls, e.g. by costly centrifugation or membrane filtration.
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Pred. No. 2.3;
2; Mismatches 0; Indels
                                                                                                                                                 Epidermal growth factor; EGF; isolation; recombinant; ion exchange chromatography; Bacillus brevis.
                                                                                                                                                                                                                                                                                                                                                                                                                             fluidised-bed ion-exchange chromatography
                                                                                                                      Epidermal growth factor analogue 4.
                                   AAW50140 standard; protein; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                 Warren B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB37612 standard; protein; 53 AA.
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8; Conserve
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CVIGYSGDRC
                                                                                            08-JUL-1998
                                                                                                                                                                                          Unidentified
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The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of plasmodium MSP-1.4.2, and has the same affinity for at least MSP-1.4.2, compared to natural MSP-1.1.9. The non-natural variants of and can be used to natural MSP-1.1.9. The non-natural variants of and can be used to treat malaria. The present sequence is human epidermal growth factor (EGF). This sequence was used in a sequence homology comparison with the wild-type MSP-1 protein from P. falciparum (see AAB37608), which was used to generate the variants of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast;
gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Epidermal growth factor (EGF) used in exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                      Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing malaria
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Pred. No. 2.3;
2; Mismatches 0;
                                                                                                                                                                                                                                                              Morgan W,
                                                                                                                                                                                                                                              Holder A, Birdsall B, Feeney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE15714 standard; Protein; 53 AA.
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80.0%; F
20-APR-2000; 2000WO-GB01558.
                                                              99GB-0009072.
                                                                                              99US-0311817.
                                                                                                                                                                                      (MEDI-) MEDICAL RES COUNCIL.
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18-JUL-2001; 2001WO-US22640.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 AA;
                                                                                                                                                                  N-PSDB; ABK10313
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                           18-JUL-2000;
                                       18-JUL-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                       Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU76706;
                                                                                                                           Coco WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                       The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 Ha useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immune responses against cancer by optimised immunisation schedules. The humanised form of the antibody 340 has reduced immunisation celeptor, as the original murine antibody and has increased ability to inhibit the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                               New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; epidermal growth factor; receptor; EGF; chimeric polynucleotide; directed evolution; chimeragenesis; recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 50; DB 23; Length 53; 80.0%; Pred. No. 2.3; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Encoded by TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse epidermal growth factor (EGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU76704 standard; Protein; 54 AA.
                                                                                                                                                                                                                               Example 5; Fig 12; 53pp; English.
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           21-MAY-2001; 2001WO-GB02226.
                                     19-MAY-2000; 2000GB-0011981
24-AUG-2000; 2000GB-0020794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                                                                            Durrant LG;
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33 CVIGYSGDRC 42
                                                                                 (SCAN-) SCANCELL LTD
                                                                                                                                      WPI; 2002-062384/08.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention.
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                                                                                                           Ellis JRM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU76704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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à a

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The invention describes a method of forming (MI) chimeric polynucleotides (I). The method comprises contacting a population of angle stranded scaffold fragments (SF) with population of donor fragments (DF) to form a complex (II) comprising at least one SF hybridised to two DFs. (II) streated so that single stranded regions of (II) are filled in and adjacent fragments are ligated. (MI) is useful for a directed evolution process which involves forming a library of (I) that can be screened for a characteristic of interest. Subsequent rounds of directed evolution can produce chimeric polynucleotides with an improved characteristic of interest. The methods facilitate the canceration of chimeric polynucleotides and do not require hybridising donor fragments to a target or full-length template. Because the chimeragenesis process does not rely upon a contiguous, full-length template, it is unnecessary to modify a template to facilitate its removal. This is the amino acid sequence of the mouse epidermal growth factor (EGF) used to demonstrate a method of in vitro recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Forming chimeric polynucleotide by contacting single-stranded (ss) scaffold fragment, and donor fragment populations to form hybridised complex having ss regions which are filled-in, and ligating adjacent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified mouse epidermal growth factor (EGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             described in the method of the invention.
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                                                                                                                                                                                                                                                  Arensdorf JJ;
                                                                                                                                                                 (ENCH-) ENCHIRA BIOTECHNOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU76706 standard; Protein; 54 AA.
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80.0%; I
2000US-219085P.
2000US-0691873.
                                                                                19-OCT-2000; 2000US-0692732
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24-JAN-2002.

us-09-673-785d-13.jull.rag

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The invention describes a method of forming (MI) chimeric
conjuncteotides (I). The method comprises contacting a population of
conjuncteotides (I). The method comprises contacting a population of
conjuncted evolution form a complex (II) comprising at least one SF
conjunction and adjacent fragments are ligated. (MI) is useful for the filled in and adjacent fragments are ligated. (MI) is useful for a directed evolution process which involves forming a library of (I)
conjuncted evolution can produce chimeric polynucleotides with an office confunction of chimeric polynucleotides and do not require hybridising confunction of chimeric polynucleotides and do not require hybridising confunction of chimeric polynucleotides and do not require hybridising confunction of chimeric polynucleotides and do not require hybridising confunction of chimeric polynucleotides and do not require hybridising confunction of chimeric polynucleotides and do not require hybridising confunction of chimeric polynucleotides and do not require hybridising confunction of chimeric polynucleotides and contiguous, full-length confunction confined it is unnecessary to modify a template to facilitate its conformation described in the method of in vitro protein (AAU76705) and used to demonstrate a method of in vitro
                                                                                                                                                                                                                                                                                                                                                Forming chimeric polynucleotide by contacting single-stranded (ss) scaffold fragment, and donor fragment populations to form hybridised complex having ss regions which are filled-in, and ligating adjacent
                                                                                                                                                                                              (ENCH-) ENCHIRA BIOTECHNOLOGY CORP.
                                                                                                                                                                                                                                     Coco WM, Encell LP, Arensdorf JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 3; 65pp; English.
                                                                                   18-JUL-2000; 2000US-218921P.
18-JUL-2000; 2000US-219085P.
19-OCT-2000; 2000US-0691873.
19-OCT-2000; 2000US-0692732.
                                         18-JUL-2001; 2001WO-US22640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0%; I
Matches 8; Conservative 2;
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N-PSDB; ABK10315.
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; Score 50; DB 23; Length 54; Pred. No. 2.3; 2; Mismatches 0; Indels 1 CVIGXSGDXC 10 33 CVIGYSGDRC 42 δλ g

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Indels

Search completed: July 2, 2003, 07:30:55 Job time: 43.3333 secs

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          GenCore version 5.1.6
Copyright (c) 1993 + 2003 Compugen Ltd.
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                                                                                                                                                                         262574 seqs, 29422922 residues
                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               OM protein - protein search, using sw model
                                                                                                                                            BLOSUM62DX
Gapop 10.0 , Gapext 0.5
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                                                                                                       US-09-673-785D-13
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1 CVIGXSGDXC 10
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                                                                                                        Title:
Perfect score:
                                                                                                                            Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*

Issued_Patents_AA:*

Database

STIMMARTES

	Description	Sequence 7, Appli	7	7	N		Patent No. 5180808	Sequence 16, Appl	19,	19,	1, 2	10,	10,	10,	. 533	Sequence 2, Appli		Š.	Patent No. 5256643	Sequence 14, Appl	14,	Sequence 44, Appl	24,	12,	Н	Sequence 17, Appl	17,	Sequence 15, Appl
SUMMARIES	ID	US-08-597-545-7	US-08-457-135-7	US-08-284-923-2	US-08-619-032B-2	5332669-2	5180808-2	US-08-185-432-16	US-08-083-590A-19	US-08-532-384-19	US-08-899-232-1	US-09-191-647-10	US-09-540-245A-10	US-09-540-153-10	5332669-1	US-08-525-864A-2	5183805-1	5183805-2	5256643-8	US-08-039-364-14	US-09-158-710-14	US-08-168-091A-44	US-08-278-089A-24	US-08-899-437-12	US-09-126-121-12	US-08-753-007A-17	US-09-398-496-17	US-09-020-880-15
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ď	Ouery Match	100.0	100.0	100.0	100.0	100.0	86.0	86.0	86.0	86.0	86.0	84.0	84.0	84.0	80.0	80.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0
	Score	20	20	20	20	20	43	43	43	43	43	42	42	42	40	40	39	39	39	39	39	39	38	39	39	39	39	39
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48 4 US-08-91 48 4 US-09-10 48 4 US-09-10 48 6 5171197-55 53 1 US-08-28 53 1 US-08-28 53 2 US-08-86 53 4 US-08-86 53 4 US-08-86 53 6 5434135-55 6 5434135-65 53 6 5434135-91 1 US-07-84 91 2 US-08-45		1 n	Length 12 0; Indels
	US-08-915-096A-1 US-09-101-544-15 5434135-3 5177197-50 US-07-869-176-1 US-08-289-23-1 US-08-861-000-1 US-08-861-000-1 US-08-861-000-1 US-08-861-000-1 US-08-81-000-1 US-08-81-000-1 US-08-81-000-1 US-08-81-000-1 US-08-81-000-1 US-08-81-000-1 US-08-81-000-1 US-08-81-000-1 US-08-81-000-1 US-08-81-000-1 US-08-81-000-1 US-08-81-000-1	Gene cine suit Suit \$ 9,537	Score 50; DB Pred. No. 0.11; 2; Mismatches
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SOUTH THE PARTY OF		IS-08-597-545-7 Sequence 7, Ap; Patent No. 558 GENERAL INFORA APPLICANT: TITLE OF IN COMPUTER: TELEPAN: FILING DA APPLICATING DA APPLICATING DA TELEFAN: TELEPAN: TELEPA	Match Scoral Ses 8

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Sequence 2, Application US/08619032B

Fatent No. 6191106

GENERAL INFORMATION:
APPLICANT: Mullenbach, Guy T.
APPLICANT: Blancy, Jeffrey M.
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: MOTEINS OF EPIDERMAL GROWTH FACTOR
TITLE OF INVENTION: EXHIBITING ENHANCED BINDING AT LOW PH
NUMBER OF SEQUENCES: 3
CORRESPONDENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: Intellectual Property R-440, P.O. Box 8097
CITT: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 50; DB 1; Length 53; 80.0%; Pred. No. 0.44;
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MEDIUM TYPE: Floppy disk
COMPUTER: INPOPY disk
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SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: 20.4MR-1996
FILING DATE: 20.4MR-1996
CLASSITCATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: Guth, Joseph H.
REGISTRATION NUMBER: 031.201
PROFINEMATION NUMBER: 0331.004
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.44
2; Mismatches
                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/746,651
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BALBARA G
REGISTRATION NUMBER: 231.01
TELECHONE 510-601-2708
TELECHONE: 510-601-2708
TELEFRAX: 510-65-3542
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 0231.004
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 53 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (510) 655-3542
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-284-923-2
                                                                                                                                                                                                                                                                                                                                                                                                         single
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                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Eme:
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
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APPLICANT: Mullenbach, Guy T
APPLICANT: Blaney, Jeffrey M
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: Exhibiting enhanced binding at low ph
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Chiron Corporation
STREET: 4560 Horton street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                      Sequence 7, Application US/08457135
Fatent No. 5644031
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FAPLICANT: LABORDA, Jorge
TITLE OF INVENTION:
FAPLICANT: LABORDA, Jorge
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE:
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,135
FILING DATE: 01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 01-JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/989,537
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.11
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50;
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08284923
Patent No. 5547935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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STATE: CA
                      US-08-457-135-7
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Gaps

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REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
TELEBHONE: 212 8698864/9741
TELEFAX: 212 8698864/9741
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LENGTH: 2471 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-185-432-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                      :: New York
'RY: U.S.A.
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York COUNTRY: U.S.A. ZIP: 10036
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                                       New York
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                                                    STATE: No COUNTRY:
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Patent No. 5750652
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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** TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID

** SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN

** ANTIBODIES, ANTI METHOD OF DETECTING THE SAME

** NUMBER OF SEQUENCES: 4

** CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 53;
                                                                      DB 4; Length 53;
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70.0%; Pred. No. 1.7e+02;
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Pred. No. 0.44;
2; Mismatches
                                                                                                                                                                                                                                                           Patent No. 5332669
; APPLICANT: DEUEL, THOMAS F.
; TITLE OF INVENTION: PROSTATE-DERIVED MITOGEN
                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                      Score 50;
                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/441,179 FILING DATE: 27-NOV-1989
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/356,739
FILING DATE: 24 MAR-1989
                                                                    100.0%;
80.0%; F
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80.0%; F
                                                                 Query Match 100.
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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Matches 7; Conservative
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2128 CVPGYSGDQC 2137
                , MOLECULE TYPE: protein US-08-619-032B-2
                                                                                                                                                             33 CVIGYSGDRC 42
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                                                                                                                                         1 CVIGXSGDXC 10
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2409
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                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 53
5332669-2
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US-08-185-432-16
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Sequence 19, Application US/08083590A
Patent No. 5786158
GENERAL INFORMATION:
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And TITLE OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/185,432 FILING DATE: 21-JAN-1994 CLASSIFICATION: 530 YITORNEY Account
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 1; 1
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/083,590A FILLING DATE: 25-JUN-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                             FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-C
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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70.0%;
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Sequence 1, Application US/08899232
Patent No. 6436650
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ATTAVATION:
APPLICANT: Q1, Hullin
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
FILE REFERENCE: 7326-046
CURRENT APPLICATION NUMBER: US/08/899,232
CURRENT FILING DATE: 1997-07-23
NUMBER OF SEO ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
Sequence 10, Application US/09191647
Fatent No. 6046015
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Bross, Katja
APPLICANT: Bross, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modilating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT APPLICATION NUMBER: 60/065,544
EARLIER RILING DATE: 1997-11-14
EARLIER FILING DATE: 1997-11-14
SEARLIER FILING DATE: 1997-11-14
SARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
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Patent No. 6270984
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 4; 1
Pred. No. 1.7e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 3;
Pred. No. 18;
5; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                            86.0%;
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50.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CVIGXSGDXC 10
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVIGXSGDXC 10
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11 CMLGYTGDNC 20
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                                                                                                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 2471
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US-09-540-245A-10
                                        RESULT 10
US-08-899-232-1
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Patent No. 6083904
Patent No. 6083904
APPLICANT: Artavanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
NUMBER OF SEQUENCES: 21
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                                                                                                                                                                                                         Length 2471;
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                                                                                                                                                                                                     Score 43; DB 1; Length 247
Pred. No. 1.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7326-015
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/083,590
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 mino acids
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 anino acids
                                                                                                                                                                                                 Query Match 86.0%;
Best Local Similarity 70.0%;
Matches 7; Conservative ;
                                                                                                                        ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-19
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                        single
                                                                                                                                                                                                                                                                                                     326 CVNGWSGDDC 335
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                                                                                                                                                                                                                                                                               1 CVIGXSGDXC 10
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                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
: U.S.A.
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                                                                                                  STRANDEDNESS:
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Gaps

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Length 154;

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Gaps

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Length 2471;

Gaps

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GENERAL INFORMATION:
APPLICANT: Chang, Han
TITLE OF INVENTION: Cerebellum-derived Growth Factors, and Uses
TITLE OF INVENTION: Related thereto
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Massachusetts
COUNTRY: USA
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  Indels
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USAN
ZIP: OC109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/525,864A
FILLING DATE: 8-SEP-1995
CLASSIFICATION: 530
ATTORNEY, AGENT INFORMATION:
NAME: KATA, CATHERIAN 41,106
REGISTRATION NUMBER: 41,106
RECISTRATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: July 2, 2003, 07:25:44 Job time : 12 secs
                                                                                                                                                                                              Sequence 2, Application US/08525864A Patent No. 5912326
  3;
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50.0%;
  6; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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                                         1 CVIGXSGDXC 10
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33 CVIGYIGERC 42
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US-08-525-864A-2
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  Matches
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APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPRESINCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/191,647
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-04-07
                                                                                                                                                                                                                                                                                                                              Score 42; DB 4; Length 154; Pred. No. 18;
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5332669-1
; Patent No. 5332669
; APPLICANT: DEUEL, THOMAS F.
; TITLE OF INVENTION: PROSTATE-DERIVED MITOGEN
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION MOMBER: US/07/356,739
: APPLICATION MOMBER: .....1;
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Pred. No. 12;
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Pred. No. 18;
5; Mismatches
           CURRENT APPLICATION NUMBER: US/09/540,245A;
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/09540153
Patent No. 6270995
BERRAL INFORMATION:
APPLICANT: Goodman, Corey
                                                                                                                                                                                                                                                                                                                              84.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%;
60.0%;
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50.0%;
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 50.0°
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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11 CMLGYTGDNC 20
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11 CMLGYTGDNC 20
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Best Local Similarity
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                                                                                                                                                                                                                                                              ORGANISM: mouse
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US-09-540-153-10
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TYPE: PRT
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2003, 07:28:49 ; Search time 103 Seconds (without alignments) 11.164 Million cell updates/sec July Run on:

US-09-673-785D-13 50 Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

1 CVIGXSGDXC 10

440863 segs, 114992915 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_AA: Database :

/cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
 /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 19, Appl	Sequence 33, Appl	Sequence 30, Appl	ď	Sequence 930, App	Sequence 7, Appli	'n	Sequence 4, Appli	Sequence 20, Appl	Sequence 4, Appli	Sequence 171, App	٦.	Sequence 12, Appl	Sequence 12, Appl	Sequence 12, Appl	17,	3, A	Sequence 9, Appli	
ID	US-10-138-158-19	US-10-150-648B-33	US-10-150-648B-30	US-10-024-599-4	US-09-925-301-930	US-09-900-449A-7	US-09-900-449A-5	US-09-900-449A-4	US-10-211-994-20	US-09-864-675-4	US-10-157-031-171	US-10-136-573A-12	US-09-877-665-12	US-10-215-862-12	US-09-817-647-12	US-10-096-241-17	US-10-201-945-13	US-09-903-327A-9	US-10-150-648B-35
DB	6	σ	σ	6	10	σ	σ	σ	σ	10	δ	6	0	σ	10	12	σ	σ	σ
å Query Match Length DB	53	53	145	176	741	572	601	639	112	298	878	46	46	46	46	47	48	53	53
& Query Match	100.0	100.0	100.0	86.0	86.0	84.0	84.0	84.0	80.0	80.0	80.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0
Score	50	20	20	43	43	42	42	42	40	40	40	39	39	39	39	39	39	39	39
Result No.		7	m	❖	S	ø	7	80	6	10	11	12	13	14	15	16	17	18	19

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Sequence 4, Appli Sequence 31, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 5, Appli Sequence 7, Appli Sequence 7, Appli Sequence 64, Appli Sequence 692, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1126, Appli Sequence 1126, Appli Sequence 1126, Appli Sequence 1126, Appli Sequence 1126, Appli Sequence 213, Appli Sequence 213, Appli Sequence 213, Appli Sequence 214, Appli Sequence 226, Appli Sequence 226, Appli Sequence 226, Appli Sequence 226, Appli Sequence 226, Appli	
9 US-10-211-994-4 10 US-09-848 664-31 0 US-09-934-706-3 9 US-10-02-934-706-3 9 US-10-211-994-29 9 US-10-211-994-29 9 US-10-211-994-5 9 US-10-211-994-5 9 US-10-211-994-5 10 US-09-280-030-64 9 US-10-211-994-5 10 US-09-280-030-64 9 US-10-280-986-050A-692 9 US-09-286-050A-692 9 US-09-286-050A-692 9 US-09-790-264-15 10 US-09-790-264-15 10 US-09-790-264-15 10 US-09-995-593A-42 10 US-09-995-693A-9	
53 58 58 68 62 62 62 62 62 62 62 62 62 62 62 62 62	
6 4 4 4 4 7 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8	

ALIGNMENTS

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PUBLICATION NO. US.CUGJOUSDOJAL

GENERAL INFORMATION:
APPLICANT: TUAREZIK, Daniel R.
APPLICANT: TUAREZIK, Daniel R.
APPLICANT: TUAREZIK, Daniel R.
APPLICANT: PERRET, Addre
APPLICANT: PERRET, Stefan
APPLICANT: PASKELL, Stefan
APPLICANT: RENO, John M.
TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS AND METHODS OF U
FILE REFERENCE: STEMI110-6
CURRENT APPLICATION NUMBER: US/10/138,158
CURRENT APPLICATION NUMBER: US 09/641,587
PRIOR APPLICATION NUMBER: US 09/559,248
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 1000-04-26
PRIOR FILING DATE: 1000-01-27
PRIOR PILING DATE: 1000-01-27
PRIOR PILING DATE: 1000-01-27
PRIOR APPLICATION NUMBER: US 09/459,813
PRIOR FILING DATE: 1000-01-27
PRIOR PILING DATE: 1000-01-27
PRIOR APPLICATION NUMBER: US 09/378,567
PRIOR PILING DATE: 1000-01-27
PRIOR PILING DATE: 1000-01-27
PRIOR PILING DATE: 1000-01-27
PRIOR APPLICATION NUMBER: US 09/378,567
PRIOR PILING DATE: 1000-01-27
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Pred. No. 0.51;
2; Mismatches 0; Indels
Sequence 19, Application US/10138158 Publication No. US20030036509A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
80.0%; F
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Best Local Similarity 80.0
Matches 8; Conservative
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; ORGANISM: Homo sapiens
US-10-138-158-19
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; DATABASE ACCESSION NUMBER: GenBank Accession No. US20030059802Al J00380; DATABASE ENTRY DATE: 1993-04-27; RELEVANT RESIDUES: Relevant residues FROM 919 TO 1063
US-10-150-648B-30
                                                                                                                                                                                   Gaps
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| Patent No. US20020052308A1
| Patent No. US20020052308A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PA106
| CURRENT APPLICATION NUMBER: US/09/925,301
| PRIOR APPLICATION NUMBER: US/09/925,301
| PRIOR APPLICATION NUMBER: 60/124,270
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1694
| SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                      Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 176;
                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                             Sequence 4: Application US/10024599
Patent No. US20020165352A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Glmbora, Daniel M.
APPLICANT: Hetchman, Karen.
APPLICANT: Hetchman, Karen.
APPLICANT: Bartel, Paul L.
TITLE OF INVENTION: Protein-Protein Interactions
FILE REFERENCE: 2318-278-II
CURRENT APPLICATION NUMBER: US/10/024,599
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/256,986
PRIOR FILING DATE: 2000-12-21
                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 9;
Pred. No. 18;
2; Mismatches
                                                                                                                                      100.0%; Score 50; DB 80.0%; Pred. No. 1.3; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: Xaa is Gly or Cys US-10-024-599-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.0%;
70.0%;
                                                                                                                                      Query Match 100.
Best Local Similarity 80.0
Matches 8; Conservative
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Matches 7; Conservative
                                                                                                                                                                                                                                                1 CVIGXSGDXC 10
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE LOCATION: 1..176
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NAME/KEY: SITE
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LENGTH: 741
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                                                                                APPLICANT: John, Sushil J.
APPLICANT: Belinger, Leonard B.
APPLICANT: Benkel, Bernhard F.
TITLE OF INVENTION: Nucleic acid and protein sequences of bovine epidermal growth FILE REFERENCE: 60-01
CURRENT APPLICATION NUMBER: US/10/150,648B
PRIOR APPLICATION NUMBER: 60/292,136
PRIOR PLING DATE: 2001-05-18
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JATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: Relevant residues FROM 977 TO 1029
US-10-150-648B-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Gray, A., Dull, T.J. and Ullrich, A. TITLE: Nucleotide sequence of epidermal growth factor cDNA predicts a TITLE: 128,000-molecular weight protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
AUTHORS: Gray, A., Dull, T.J. and Ullrich, A.
TITLE: Nucleotide sequence of epidermal growth factor cDNA predicts of TITLE: Nucleotide sequence of epidermal growth factor cDNA predicts of JOURNAL: Nature
VOLUME: 303
BAGES: 722-725
DATE: 1983
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US-10-150-648B-30
US-10-150-648B-30
Sequence 30, Application US/10150648B
Publication No. US20030059802A1
GENERAL INFORMATION:
APPLICANT: Bllodeau-Goesseels, Sylvie
                                         Sequence 33, Application US/10150648B Publication No. US20030059802Al GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 CVIGYSGDRC 42
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PUBLICATION INFORMATION
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RESULT 2
US-10-150-648B-33
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PAGES: 722-725
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APPLICANT: ZHONG, Jenny et al.

TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL001271

CURRENT APPLICATION NUMBER: US/09/900,449A

CURRENT FILING DATE: 2001-07-09

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Nucleotide and peptide sequence of multivalent vaccine US-10-211-994-20
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Sequence 20, Application US/10211994

Publication No. US20030082201A1

Sequence 20, Application World

Publication No. US20030082201A1

SERNERAL INFORMATION:

APPLICANT: Rao, M.R.S.

APPLICANT: Prasad, Sudhanand

APPLICANT: Burman, Anand C.

APPLICANT: Homes, Becky

TILLE OF INVENTION: MULTIVALENT SYNTHETIC VACCINE FOR CANCER

FILE REFERENCE: 1014152-1

CURRENT FILING DATE: 2002-08-02
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84;
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60.0%; Pred. No. 35;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 9
Pred. No. 84;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Strongylocentrotus purpuratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/309,975
PRIOR FILING DATE: 2001-08-03
                                                                                                        Sequence 4, Application US/09900449A Publication No. US20030040616A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09864675 Patent No. US20020081286A1
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SOFWARE: Patentin version 3.1
SEQ ID NO 20
ENGTH: 112
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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92 CVIGYIGERC 101
                 132 CPLGFSGDNC 141
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60 CPLGFSGDNC 69
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                                                                           RESULT 8
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Publication No. US20030040616A1
GENERAL INFORMATION:
APPLICANT: ZHONG, Jenny et al.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USSE THEREOF
FILE REFERENCE: CLO01271
CURRENT APPLICATION NUMBER: US/09/900,449A
CURRENT PILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09900449A
Publication No. US20030040616A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/900,449A
CURRENT PILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
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                               NAME/KEY: SITE
LOCATION: (19)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                           NAME/KEY: SITE

1. LOCATION: (282)

2. COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-930
                 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                             1; Indels
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Pred. No. 76;
3; Mismatches
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Pred. No. 79;
3; Mismatches
                                                                                                                                                                                      Score 43; DB 1
Pred. No. 67;
2; Mismatches
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60.0%;
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60.0%;
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Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity bu.v.
6; Conservative
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Best Local Similarity 60.00
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141 CPLGFSGDNC 150
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460 CVPGYSGDQC 469
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US-09-900-449A-7
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US-09-900-449A-5
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LENGTH: 601
LOCATION:
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US-09-877-665-12
Sequence 12, Application US/09877665
Fatent No. US20020164680al
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
IITLE OF INVENTION:
Ligands and Uses Therefor
                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                 DB 9; Length 46;
22;
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COMPUTER READABLE FORM:
COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MinPatin (Genentech)
APPLICATION DATA:
APPLICATION NUMBER: US/09/877,665
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/09/109,206
FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 9;
Pred. No. 22;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: COnley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-877-665-12
                                                                                                                                                                                                      Score 39;
Pred. No.
    PRIOR FILING DATE: 1997-07-24
PRIOR APPLICATION NUMBER: US 60/052,019
PRIOR FILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 12
LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650/225-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 46 amino acids TYPE: Amino Acid
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50.0%;
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50.0%;
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                           Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                               1 CVIGXSGDXC 10
                                                                                                                                                                                                                                                                                                      32 CVVGYIGERC 41
                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-136-573A-12
                                                                                                                                                                             Query Match
Best Local Similarity.
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                                                                                                                        TYPE: PRT
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APPLICANT: Yankovsky, N. K.
APPLICANT: Lobashev, A. P.
APPLICANT: Lobashev, A. V.
TITLE OF INVENTION: In Silico screening for phenotype-associated expressed sequences FILE REFERENCE: 2760-103
CURRENT APPLICATION WIMBER: US/10/157,031
CURRENT APPLICATION WIMBER: US/10/157,031
SOFTWARE: PATELING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 878
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            APPLICANT: Marchionni, Mark
TITLE OF INVENTION: NRG-2 NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: POLYEPPTIDES, AND DIAGNOSTIC AND THERAPEUTIC METHODS
CURRENT ELICE OF 10455/049002
CURRENT APPLICATION NUMBER: US/09/864,675
CURRENT FILLING DATE: 2001-05-23
PRIOR PILLING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020161200A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOOWSKI, Paul J.
APPLICANT: Zhang, Dong Xiao
TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related Ligands and
FILE REFERENCE: P1084RIC2
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                                                                                                                                                                                                                                                                                                                                  Length 298;
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                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                  Score 40; DB 10;
Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 9; 1
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/136,573A CURRENT FILING DATE: 2002-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/480,977
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 08/899,437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 171, Application US/10157031
Publication No. US20030108890A1
GENERAL INFORMATION:
APPLICANT: Baranova, A. V.
APPLICANT: Yankovsky, N. K.
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                1 :|::||:|
280 CPVGYTGDRC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: |:||:|
526 CLPGFSGDRC 535
                                                                                                                                                                                                                                                                                                                                                                                                            1 CVIGXSGDXC 10
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                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-09-864-675-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-157-031-171
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-10-157-031-171
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US-10-136-573A-12
                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 298
                                                                                                                                                                                                                                                     TYPE: PRT
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Search completed: July 2, 2003, 07:57:19 Job time : 104 secs
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32 CVVGYIGERC 41
                                                                                                     FEATURE
                                                                                                                                                                                                                          US-09-817-647-12
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                     RESULT 14

US-10-215-862-12

Jeaquence 12, Application US/10215862

Publication No. US20030036166A1

GENERAL INFORMATION:

APPLICANT: GAOWSKI, Paul J.

APPLICANT: Abang, Dong Xiao

TITLE OF INVENTION: USES Therefor

TITLE OF INVENTION: USES Therefor

FILE REFERENCE: P1084R1D2C1

CURRENT APPLICATION NUMBER: US/10/215,862

CURRENT APPLICATION NUMBER: US 09/126,663

PRIOR FILING DATE: 1998-07-30

PRIOR FILING DATE: 1997-07-24

PRIOR PLING DATE: 1997-07-24

PRIOR PLING DATE: 1997-07-09

SEQ ID NO 12

LENGTH: 46

LENGTH: 46
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TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
Ligands and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 9; Length 46; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/817,647
FILING DATE: 26-MAT-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/107,979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09817647; Patent No. US20020082229A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650/952-988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.0
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CVIGXSGDXC 10
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32 CVVGYIGERC 41
32 CVVGYIGERC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-10-215-862-12
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US-09-817-647-12
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LOCATION: 1-46
LDENTIFICATION METHOD:
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                  SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                hEGF.egf
                                                                                                                NAME/KEY:
```

Score 39; DB 10; Length 46; Pred. No. 22; 4; Mismatches 1; Indels 78.0%; 50.0%; Query Match 78.0 Best Local Similarity 50.0 Matches 5; Conservative

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1 CVIGXSGDXC 10

CID

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments)
80.112 Million cell updates/sec 2, 2003, 07:25:01; Search time 12 Seconds July

Run on:

US-09-673-785D-13 50 1 CVIGXSGDXC 10 Perfect score: Sedneuce: BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Potal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq.length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pirl:* pir2:* pir3:* PIR 73:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	epidermal growth f		probable tenascin	chondroitin sulfat	hypothetical prote	versican - pig-tai	Motch B protein -	versican precursor	versican precursor	cell-fate determin	notch homolog - se	versican precursor	fibropellin Ia - s	Notch homolog prot		neuroendocrine pro	probable potassium	epidermal growth f	slit-1 protein hom	transmembrane prot	hypothetical prote		hypothetical prote		_		pr	gene Delta protein	neurogenic repetit
SUMMAKIES	. di	EGMSMG	A35672	T09070	B55885	T29359	S43922	A49175	T14274	A60979	A49128	T31070	T42389	A40136	T30201	PC4415	803938	T48539	EGRT	T42218	S42612	T16271	T16213	S74581	AH1831	F85164	T34396	A31246	S19087	200670
	DB	-	7	7	~	N	ď	ď	N	,	~	7	7	7	7	~	~	~	Н	~	~	N	7	~	7	7	7	7	7	7
	Length	1217	2139	4006	102	372	862	1203	1643	2409	2471	2531	3381	1064	2352	27	161	601	1133	1531	2437	264	379	422	426	470	601	832	833	880
d	Query Match	100.0	90.0	90.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	84.0	82.0	80.0	80.0	80.0	80.0		80.0	78.0	78.0	78.0	78.0	78.0	78.0	٠	78.0	78.0
	Score	50	45	45	43	43	43	43	43	43	43	43	43	42	41	40	40	40	40	40	40	39	39	39	39	39	39	39	39	39
٠	Result No.	7	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25		27	28	29

brevican precursor	ATP-dependent perm	epidermal growth f	protein F11C7.4 (i	versican precursor	hypothetical prote	zonadhesin - pig	tenascin-X precurs	tenascin-X - bovin	hypothetical prote	bacitracin synthet	hydrophobin Ccg-2	hypothetical prote	conserved hypothet	hypothetical prote	mucin - rat (fragm
849126	S19421	EGHU	E89753	A55535	T22759	T34022	A40701	T42629	T20721	T31677	A46222	E98236	AF3049	T22300	A39321
7	Н	Н	~	Н	7	~	-	7	~	~	7	~	7	7	7
883	1049	1207	1722	2397	2824	2476	3566	4135	4307	5255	108	294	294	373	447
78.0	78.0	78.0	78.0	78.0	78.0	76.0	76.0	76.0	76.0	76.0	74.0	74.0	74.0	74.0	74.0
39	39	39	39	39	39	38	38	38	38	38	37	37	37	37	37
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1	_
EGMSMG	_
epidermal growth factor precursor - mouse	
N;Alternate names: urogastrone precursor	
C;Species: Mus musculus (house mouse)	_
C;Date: 30-Nov-1980 #sequence_revision 11-Aug-1983 #text_change 19-Jan-2001	
C; Accession: A94272; A93304; A92118; A01387	
R; Scott, J.; Urdea, M.; Quiroga, M.; Sanchez-Pescador, R.; Fong, N.; Selby, M.; Ruti	ũ
Science 221, 236-240, 1983	_
A; Title: Structure of a mouse submaxillary messenger RNA encoding epidermal growth	,-
A; Reference number: A94272; MUID:83223630; PMID:6602382	
A;Accession: A94272	
A; Molecule type: mRNA	
A; Residues: 1-1217 <sco></sco>	
A; Cross-references: GB:J00380; NID:q192993; PIDN:AAA37539.1; PID:q309210	
R; Gray, A.; Dull, T.; Ullrich, A.	
Nature 303, 722-725, 1983	
A; Title: Nucleotide sequence of epidermal growth factor cDNA predicts a 128,000-mol	_
A; Reference number: A93304; MUID:83219309; PMID:6304537	-
1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	

A; Accession: A93304

A; Note: the sequence shown by these authors differs from residues 1134-1168 due to A;Molecule type: mRNA A;Residues: 1-789,'Y',791-1047,'S',1049-1168 <GRA> A;Cross-references: GB:J00380

A.You control of Scott et al.)

R.Savage Jr., C.R.; Inagami, T.; Cohen, S.

J. Biol. Chem. 247, 7612-7621, 1972

A.Feference number: A92118; MUID:73048516; PMID:4636327

A.Ancession: A92118; MUID:73048516; PMID:4636327

A.Molecule type: protein

A.Molecule type: protein

A.Molecule type: protein

A.Molecule type: protein

A.Residues: 977-1029 <SAV>
A.Note: residues 1024-1029 are not required for full biological activity in vivo

R.Savage Jr., C.R.; Hash, J.H.; Cohen, S.
J. Biol. Chem. 248, 7669-7672, 1973

A.Fitle: Epidermal growth factor. Location of disulfide bonds.

A.Reference number: A92144; MUID:7405498; PMID:4750422

A.Contents: annotation; disulfide bonds

C; Comment: Epidernal growth factor (EGF) stimulates the proliferation and different gastrointestinal call proliferation.
C; Comment: EGF is released in the pancreas, small intestine, mammary gland, and (in C; Comment: The EGF precursor is found in kidney as a receptor-like membrane-bound po C; Comment: The active growth factor from this submaxillary gland protein stimulates

C; Superfamily: epidermal growth factor precursor; EGF homology; LDL receptor VWTD-cc (Keywords: duplication; growth factor; tandem repeat; transmembrane protein F;1-28/Domain: signal sequence #status predicted <SIG> F;29-1217/Product: epidermal growth factor proprotein, membrane-bound form #status ; F;29-1038/Domain: extracellular #status predicted <EXT> F;30-48/FRegion: EGF precursor long repeat F;53-92/Domain: LDL receptor YWTD-containing repeat homology <YW01> F;93-134/Domain: LDL receptor YWTD-containing repeat homology <XW02> . C;Superfamily:

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C; Accession: T09070
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region A;Reference number: 216543
A;Accession: T09070
A;Status: prealininary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-4006 < ROW>
A;Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A map position: 17
A: Map position: 17
A: Introns: 124/1; 735/1; 773/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 144C/1;
A: Introns: 124/1; 735/1; 773/3; 826/1; 317/1; 3558/1; 3606/1; 3606/1; 3606/1; 3606/1; 3727/3; 2506/1; 3108/1; 3102/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3105/1; 3
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chondroitin sulfate proteoglycan MV3 - human (fragment)
C;Species: Homo sapiens (man)
S;Zako, M.; Shinomura, T.; Ujita, M.; Ito, K.; Kimata, K.
J. Biol. Chem. 270, 3914-3918, 1995
A;Title: Expression of PG-M(V3), an alternatively spliced form of PG-M without a choracession: B55885
A;Reference number: A55885; MUID:95181355; PMID:7876137
A;Reference number: A55885
A;Reference number: A55885
A;Molecule type: mRNA
A;Residues: 1-102 <ZAK>
A;Crass_references: GB:575879; GB:D32039
A;Cross_references: GB:575879; CB:D32039
C;Superfamily: versican; C-type lectin homology; complement factor H repeat homolcgy, F;24-55/Domain: EGF homology <EG2>
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C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: 129359
R; Murray, J.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A; Description: The sequence of C. elegans cosmid R05G6.
A; Reference number: 220612
A; Accession: T29359
                                                    probable tenascin X - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 2.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.0%;
70.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: INX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
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                                                                      F;11/7-11/Domain: LDL receptor YWTD-containing repeat homology <rw>
F;218-262/Domain: LDL receptor YWTD-containing repeat homology <rw>
F;248-262/Domain: LDL receptor YWTD-containing repeat homology <rw>
F;248-360/Domain: EGF homology & #status atypical <EGI>
F;364-360/Domain: EGF homology <EG3>
F;465-442/Domain: EGF homology <EG3>
F;465-442/Domain: EGF homology <EG3>
F;465-482/Domain: EGF precursor long repeat homology <rw>
F;486-961/Region: EGF precursor long repeat homology <rw>
F;486-951/Domain: LDL receptor YWTD-containing repeat homology <rw>
F;530-512/Domain: LDL receptor YWTD-containing repeat homology <rw>
F;513-615/Domain: LDL receptor YWTD-containing repeat homology 
F;616-659/Domain: LDL receptor YWTD-containing repeat homology 
F;616-659/Domain: LDL receptor YWTD-containing repeat homology 
F;616-6700/Domain: EGF homology <EG5>
F;841-875/Domain: EGF homology <EG5>
F;841-875/Domain: EGF homology <EG6>
F;841-875/Domain: EGF homology <EG8>
F;937-1029/Product: epidermal growth factor #status experimental <EGF>
F;923-958/Domain: transmembrane #status predicted <INM>
F;1039-1063/Domain: intracellular *status predicted <INM>
F;341-750-350/Johain: intracellular *status predicted <INM>
F;341-750-350/Johain: intracellular *status predicted <INN>
F;341-750-350/Johain: intracellular *status predicted <INN>
F;341-350/Johain: intracellular *status predicted <INN>
F;341-750-350/Johain: intracellular *status predicted <INN>
F;341-750-350/Johain: intracellular *status predicted <INN-7-418/Johain: intracellular *status *status *status *status <INN-7-418/Johain: intracellular *status *status *status <INN-7-418/Johain: intracellular *status *status *status *status <INN-7-418/Johain: intracellular *status *status
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A; Molecule type: mRNA
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-2139 <TEP>
A; Molecule type: mRNA
A; Residues: 1-2139 <TEP>
A; Cross-references: GB:M33753
A; Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residu C; Genetics: FlyBase:FBqn0000368
A; Greetics: FlyBase:FBqn0000368
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Reywords: transmembrane protein
F; 352-385/Domain: EGF homology <EGF1>
F; 352-424/Domain: EGF homology <EGF2>
F; 691-722/Domain: EGF homology <EGF5>
F; 1878-1914/Domain: EGF homology <EGF3>
F; 1878-1914/Domain: EGF homology <EGX2>
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(Species: Drosophila melanogaster

(Species: Drosophila melanogaster

(Space: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 11-Jan-2000

(SAccession: A33672

(R) Tepass, U.; Theres, C.; Knust, E.

(B) Tepass, U.; Theres, C.; Knust, E.

(A) Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila A; Reference number: A35672; MUID:90263104; PMID:2344615
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F;982-996,990-1007,1009-1018/Disulfide bonds: #status experimental
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YWTD-containing repeat homology
YWTD-containing repeat homology
YWTD-containing repeat homology
YWTD-containing repeat homology
#status atypical <EG1>
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Pred. No. 1.6;
2; Mismatches 0
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Best Local Similarity 80.0

Matches 8; Conservative
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571 CAVGYSGDRC 580
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tes 6; Conserv
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         F;135-176/Domain:
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R;Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R. J. Biol. Chem. 273, 15758-15764, 1998
A;Title: Versican V2 is a major extracellular matrix component of the mature bovine A;Reference number: Z17954; MUID:98288320; PMID:9624174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Identification of the proteoglycan versican in aorta and smooth muscle cell, A,Reference number: S43921; MUID:95005762; PMID:7921538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 208-440;1094-1385;1910-2246 <YAO>
R; Bignami, A.; Lane, W.S.; Andrews, D.; Dahl, D.
Brain Res. Bull. 22, 67-70, 1989
A; Title: Structural similarity of hyaluronate binding proteins in brain and cartilag
         C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-1643 <SCH>
A; Cross-references: EMBL:AF060458; NID:g3253303; PID:g3253304; PIDN:AAC24360.1
A; Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Accession: T14274
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A; Residues: 1-2409 <2IM>
A; Residues: 1-2409 <2IM>
A; Cross-references: GB:X15998; NID:g37662; PIDN:CAA34128.1; PID:g37663
R; Yao, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: glycoprotein
F;1-20/Domain: stynal sequence #status predicted <SIG>
F;21-1643/main: stynal sequence #status predicted <MAT>
F;21-1643/main: versican, splice form V2 #status predicted <MAT>
F;57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate
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A;Status: prellminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                          Score 43; DB ;
Pred. No. 26;
2; Mismatches
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Pred. No. 35;
2; Mismatches
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                                                                                        EGF homology <EGF>
EGF homology <EGX2>
EGF homology <EGF3>
EGF homology <EGF3>
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Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity 70.0%;
Matches 7; Conservative
                                          homology
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1362 CVPGYSGDRC 1371
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                                 F;143-174/Domain: Ev
F;861-513/Domain: Ev
F;560-591/Domain: Ev
F;712-743/Domain: Ev
F;836-867/Domain: Ev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S06014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S43921
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                                                                                                                                                                                                                                                                                                                                                                                                                 셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 versican - pig-tailed macaque (fragments)
Nathernate names: chondroitin sulfate proteoglycan
C;Sapecies: Macaca nemestrina (pig-tailed macaque)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 16-Jul-1999
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 16-Jul-1999
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 16-Jul-1999
R;Accession: 14, 213-225, 1994
Matrix Biol: 14, 213-225, 1994
A;Title: 1dentification of the proteoglycan versican in aorta and smooth muscle cells by A;Reference number: 843921; MUID:95005762; PMID:7921538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: versican; C-type lectin homology; complement factor H repeat homology; EQ C; Keywords: chondroitin sulfate proteoglycan; extracellular matrix C; H. 37, Domain: link protein repeat homology (fragment) < LNK1> F; S8-139, Domain: link protein repeat homology < LNK2> F; 722-753, Domain: EGF homology < EG1> F; 726-753, Domain: EGF homology < EG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Comment: This protein has many EGF repeats and lin-12/Notch repeats. C; Comment: This protein is one of the neurogenic proteins controlling the decision between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: the authors translated the codon GCC for residue 50 as Val, AAG for residue 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Mus musculus (house)
C; Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 20-Sep-1999
C; Accession: A49175; PH1570; S32113
R; Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A; Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety A; Reference number: A49175; MUID:93178563; PMID:8440332
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                        A; Molecule type: DNA
A; Residues: 1-372 < MURN:
A; CESI dues: 1-372 < MURN:
A; CESI dues: 1-572 < MURN:
A; CESI dues: 1-572 < MURN:
A; Experimental source: strain Bristol N2; clone R05G6
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A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126158)
                                                                                                                                                                                                                                                                                                                                                          Gaps
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                              Score 43; DB 2
Pred. No. 8.4;
3; Mismatches
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Pred. No. 19;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-233;234-525;526-862 <YAO>A;Cross-references: EMBL:S72413
A;Note: 507-Ser was also found
                                                                                                                                                                                                                                    A; Introns: 80/1; 161/1; 245/1; 286/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Motch B protein - mouse (fragment)
                                                                                                                                                                                                                                                                                              86.0%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.0%;
70.0%;
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                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
7, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :|:||:|
CFLGWSGDSC
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A; Residues: 1-1203 <LAR>
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                                                          A; Gene: CESP:R05G6.9
A; Map position: 4
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notch homolog - sea urchin (Lytechinus variegatus)

C;Species: Lytechinus variegatus (variegatus)

C;Species: Lytechinus variegatus (variegated urchin)

C;Date: 22-0ct-1999 #sequence_revision 22-0ct-1999 #text_change 31-Jan-2000

C;Accession: T31070

R;Sherwood, D.R.; McClay, D.R.

Development 124, 3363-3374, 1997

A;Title: Identification and localization of a sea urchin Notch homologue: insights in A;Reference number: 220966; MUID:97454256; PMID:9310331

A;Accession: T31070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-3381 <SCH>
A; Residues: 1-3381 <SCH>
A; Cross-references: EMBL: AF060456; NID: 93253299; PID: 93253300; PIDN: AAC24358.1
C; Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lec C; Reywords: chondroitin sulfate proteoglycan; extracellular matrix; glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R. J. Biol. Chem. 273, 15758-15764, 1998
A;Title: Versican V2 is a major extracellular matrix component of the mature bovire A;Reference number: Z17954; MUID:98288320; PMID:9624174
A;Reference number: Z17954; MUID:98288320; PMID:9624174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule, type: mRNA
A; Residues: 1-2531 <SHE>
A; Residues: 1-2531 <SHE>
A; Cross-references: EMBL: AF000634; NID: 92570350; PID: 92570351; PIDN: AAB82088.1
C; Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              versican precursor, splice form VO - bovine
N;Alternate names: chondroitin sulfate proteoglycan
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-May-2000
C;Accession: T42389
                            A Molecule type: mRNA
A; Residues: 1-2471 <WEI>
A; Experimental source. Schwann cell
A; Note: sequence extracted from NCBI backbone (NCBIP:127811)
C; Superfamily: notch protein; ankyrin repeat homology; EGF homology
F; 264-295/Domain: EGF homology <EGF1>
F; 799-830/Domain: EGF homology <EGF2>
F; 877-908/Domain: EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 2; Length 2531;
Pred. No. 52;
3; Mismatches 1; Indels
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preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 2;
Pred. No. 51;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          <8N3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1943-1975/Domain: ankyrin repeat homology F;1976-2008/Domain: ankyrin repeat homology F;2009-2041/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                         F;1876-1908/Domain: ankyrin repeat homology F;1909-1941/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                     F;1029-1060/Domain: BGF homology <BGF>
F;1067-1098/Domain: BGF homology <BGX3>
F;1153-1184/Domain: BGF homology <BGFP3
F;1191-1222/Domain: BGF homology <BGFP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.0%;
70.0%;
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60.0%;
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Best Local Similarity 60...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 86.0
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 CVNGWSGDDC 335
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615 CPVGTSGDNC 624
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                     A; Molecule type: protein
A; Residues: 21-22, 7x, 24-37 <PE2>
A; Residues: 21-22, 7x, 24-37 <PE2>
A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIP:118884)
R; IOZZO, R.V.; NaSo, M.F.; Cannizzaro, L.A.; Wasmuth, J.J.; McPherson, J.D.
A; Title: Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chrc
A; Reference number: 154179; MUID:93122792; PMID:1478664
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A;Cross-references: GDB:127873; OMIM:118661
A;Cross-references: GDB:127873; OMIM:118661
A;Gene: GDB:Cspcared: G12-5q14
C;Superfamily: versican; C-type lectin homology; complement factor H repeat homology; F:1-20/Domain: signal sequence #status predicted <SIG>F:1-2409/Product: proteoglycan 24K core protein #status predicted <MAT>F:265-346/Domain: link protein repeat homology <LNK1>F:265-346/Domain: link protein repeat homology <LNK2>F:559-1654/Domain: chondroitin sulfate attachment #status predicted <GAG>F:2104-2175/Domain: EGF homology <EGS>F:2144-2175/Domain: EGF homology <EGS>
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Datte: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
C;Accession: A49128
R;Weinmaster, G:; Roberts, V.J.; Lemke, G.
Development 116, 931-941, 1992
A;Fitle: Notch2: a second mammalian Notch gene.
A;Fitle: Notch2: a second mammalian Notch gene.
A;Reference number: A49128
A;Accession: A49128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 251-347 <RES>
A;Cross-references: GB:S52488; NID:g263313; PIDN:AAB24878.1; PID:g263314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
   A; Reference number: A60979; MUID:89229983; PMID:2469524
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 86.0%;
Best Local Similarity 70.0%;
Matches 7; Conservative
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2128 CVPGYSGDQC 2137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Contents: brain
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Gaps

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Gaps

Gaps

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Indels

Length 1064;

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F;788-819/Domain: EGF homology <EG18>
F;864-895/Domain: EGF homology <EG219>
F;864-895/Domain: EGF homology <EG219>
F;964-895/Domain: EGF homology <EG21>
F;902-933/Domain: EGF homology <EG21>
F;902-933/Domain: EGF homology <EG21>
F;934-1064/Reg9ion: avidin-11ke
F;33-34,28-43,45-44,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,26
57,451-466,468-477,484-455/Disulfide bonds: #status predicted
F;489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,62
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Notch homolog protein - sea squirt (Halocynthia roretzi)
C; Species: Halocynthia roretzi
C; Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C; Casession: 1730201
R; Hori, S.; Saitoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.
Dev. Genes Evol. 207, 371-380, 1997
A; Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the A; Reference number: 220775
A, Accession: 130201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: PC-12 cell
C; Comment: This protein is a member of the epidermal growth factor family. It is
sting the differentiation of MDA-MB-453 cells.
C; Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology
F;1-25/Domain: EGF homology (fragment) < EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2352 <HOR>
A;Residues: 1-2352 <HOR>
A;Cross-references: EMBL:AB001327; NID:d1204472; PID:d1026501; PIDN:BAA25571.1
A;Genetics:
A;Gene: Notch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.0%; .Score 41; DB 2; Length 235
50.0%; Pred. No. 1.1e+02;
.lve 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                    Pred. No. 34;
3; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                              NiAlternate names: epidermal growth factor homolog precursor
NiContains: alternatively spliced fibropellin ID (EGFI)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 13-May-1992 #sequence_revision 17-Sep-1997 #text_change 21-Jul-2000
C;Accession: A40136; B40136; C40136; A29316; A43131
K;Polgadillo-Reproso, M. G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A;Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comment: EGR homology repeats 10-17 are spliced out in the short form (fibropellin Ib) Superfamily: Clr/Cls repeat homology; EGF homology 1-19/Domain: Signal sequence #Status predicted <SIG> 20-1064/Product: fibropellin I #status predicted <FIB> 23-54/Domain: EGF homology <EGG1b>
     F;21-3381/Product: versican, splice form VO #status predicted <WAT>
F;57,331,352,817,965,1017,1333,1393,1437,1463,1653,1974,2045,2074,2103,2263,2290,2356,26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor. Reference number: A29316; MUID:87319677; PMID:3498216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Hunt, L.T.; Barker, W.C.
FAASB J. 3, 1760-1764, 1989
A.Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.
A;Reference number: A43131; MUID:89196806; PMID:2784773
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A;Residues: 'S',280-481,786-1064 <HUR>
A;Cross-references: GB:M17421; NID:9161474; PIDN:AAA30050.1; PID:9552260
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                                                                             Length 3381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 181-251,329-370, R', 372-408, 'RA',411-441 <DE2>
                                                                                                                             Indels

    sea urchin (Strongylocentrotus purpuratus)

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A:Accession: B40136
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69;
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                                                                             Score 43;
Pred. No.
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E;218-449/Domain: EGF hc
E;256-287/Domain: EGF hc
E;332-363/Domain: EGF hc
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E;408-439/Domain: EGF hc
E;408-439/Domain: EGF hc
E;446-477/Domain: EGF hc
E;523/Domain: EGF hc
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E;520-553/Domain: EGF hc
E;560-501/Domain: EGF hc
E;560-501/Domain: EGF hc
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E;674-705/Domain: EGF hc
E;712-743/Domain: EGF hc
E;712-743/Domain: EGF hc
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A; Molecule type: mRNA
A; Residues: 1-114 <DEL>
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447 447 477 477 477 477 477 477 477 477		9999	s (Mou Metazo utheri 10090;	OM N.A 23630; rdea M utter of a m or and	OM N.A 19309; 11 T.J seque ecular 722-72	977-1 48516; Jr., y stru em. 24	BONDS. 4025498; R. Jr., 1 growth Chem. 24	Y NMR OF 18798; P G.T., Wu , Schera tructure scopy an ";	BY NMR 075811; Inagaki ensiona growth
	E WOUSE	P01132; 21-JUL-1986 (R 21-JUL-1986 (R 15-JUN-2002 (R Pro-epidermal growth factor]	EGF. Mus musculus (Mouse). Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;	SEQUENCE FR MEDLINE-832 MEDLINE-832 MEDLINE-832 SCOCT J., O SCIENCE SCIENCE 221	SEQUENCE FROM N.A. MEDLINE-83219309; PubMed-6304537 Gray A., Dull T.J., Ullrich A.; "Nuclectide sequence of epiderma 128,000-molecular weight protein	SEQUENCE OF 977-1029. MEDLINE-73048516; PubMed=4636327; Savage C.R. Jr., Inagami T., Cohen "The primary structure of epiderma ". Biol. Chem. 247:7612-7621(1972)	DISULFIDE BONDS. MEDLINE=74025498; P Savage C.R. Jr., Ha "Epidermal growth f J. Biol. Chem. 248:	JCTURE LINE=92 telione son K.D lution spectr spectr traints	TOTAL MEDLINE-93075811; Pr Kohda D., Inagaki F "Three-dimensional i
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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STRAIN-Organon-R; TISSUE-Embryo;
MEDLINE-90263104; PubMed-2344615;
Tepass U., Theres C., Knust E.;
"Crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila epithelial cells and required for organization of epithelial.";
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D -> Y (IN REF. 2).
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TISSUE-Embryo;
MEDLINE-87218537; PubMed-3107986;
Knust E., Dietrich U., Tepass U., Bremer K.A., Weigel D.,
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15-JUN-2002 (Rel. 41, Last annotation update)
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P10040;
01-MAR-1989 (Rel. 10, Created)
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Cell 61:787-799(1990).
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                                     WEDLINE-99180407; PubMed-10082370;
WEDLINE-99180407; PubMed-10082370;
WEDLINE-99180407; PubMed-10082370;
WEDLINE-99180407; PubMed-10082370;
WEDLINE-99180407; PubMed-10082370;
WEDLINE-SC., Norton R.S.;
Role of the 6-20 disulfide bridge in the structure and activity of apidermal growth factor.
The Folderial growth factor.
The Fromer and activity of a profession of the factor.
The Fromer and activity of a profession sci. 7:1738-1749(198)
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DR PIR; A01387; ECAR24116.1; -.

DR PIR; A01387; ECAR24116.1; -.

DR PDB; 1EGF; 31-JAN-94.

DR PDB; 1EFF; 31-JAN-94.

DR PDB; 1A3P; 29-JUL-98.

DR MGD; MGI; 92-JUL-98.

DR INTEFPC; IPR000018; EGF-1.

DR INTEFPC; IPR000018; EGF-1.

DR INTEFPC; IPR000018; EGF-1.

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BGF-LIKE 1 (INCOMPLETE).
BGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
BGF-LIKE 4.
BGF-LIKE 5.
EGF-LIKE 5.
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EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
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EMBL; V00741; CAA24115.1; ALT_FRAME.
EMBL; V00741; CAA24116.1; -.
     Biochemistry 31:11928-11939(1992)
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                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EGF-LIKE 2.

EGF-LIKE 3.

EGF-LIKE 5.

EGF-LIKE 6.

EGF-LIKE 7.

EGF-LIKE 8.

EGF-LIKE 9.

EGF-LIKE 10.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 12.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14.

EGF-LIKE 14.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 15.

EGF-LIKE 16.

EGF-LIKE 17.

EGF-LIKE 17.

EGF-LIKE 18.

EGF-LIKE 18.

EGF-LIKE 19.

EGF-LIKE 18.

EGF-LIKE 19.

EGF-LIKE 11.

EGF-LIKE 
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    Vaessin H., Campos-Ortega J.A.;
"EGF homologous sequences encoded in the genome of Drosophila melanogaster, and their relation to neurogenic genes.";
EMBO J. 6:761-766(1987).

-I - FUNCTION: MAY PLAY A ROLE IN THE DEVELOPMENT OF EPITHELIA, POSSIBLY FOR THE ESTABLISHMENT AND/OR MAINTENANCE OF CELL POLARITY. IT MAY ACT AS A SIGNAL.

-I - SUBCELLULAR LOCATION: Type I membrane protein.

-I - SUBCELPRIATED 10 THE CYTOPLEASHIC DOMAIN (POTENTIAL).

-I - SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
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EGF-LIKE 20.
LAMININ G-LIKE 2.
EGF-LIKE 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M33753; AAA28428.1; ALT_SEQ.
EMBL; X05144; CAA28793.1; --
PIR; B26637; B26637.
PIR; A35672; A35672.
HSSP; P00740; IEDM.
Flybase; FBgn0000368; crb.
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

O'TYPE LECTIN.

BY SIMILARITY.

BY SIMI
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             SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                           LINK 1.
LINK 2.
GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN,
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Pred. No. 4.9;
2; Mismatches
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862
862 AA;
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Matches 7; Conserv
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Yao L.Y., Moody C., Schoenherr E., Wight T.N., Sandell L.J.;
"Identification of the proteoglycan versican in aorta and smooth muscle cells by DNA sequence analysis, in situ hybridization and immunohistochemistry."

Matrix Biol. 14:213-225(1994).

-I. FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds
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DEVELOPMENTAL STAGE: Disappears after the cartilage development
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028858; 028859; 028860;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Versican core protein (Large fibroblast proteoglycan) (Chondroitin sulfate proteoglycan core protein 2) (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca nemestrina (Pig-tailed macaque).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
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SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 2 LINK DOMAINS.
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3; Mismatches
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Best Local Similarity 60.0
Matches 6; Conservative
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Gaps

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Length 862; 1; Indels

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MEDLINE-95333893; PubMed-7609614;
Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Tsujimoto Y.;
"Differential expression of Notchl and Notch2 in developing and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21374376; PubMed-11459941; Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.; "Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members."

Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

-!- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged!, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with
                                                                                                          NTC2_MOUSE STANDARD, PRT; 2470 AA.
035516; 066941; Q06008;
15-JUN-2002 (Rel. 41, created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isujimoto Y.; "Mutation in ankyrin repeats of the mouse Notch2 gene induces early
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/6; TISSUE-Thymus; Hamada Y., Higuchi M., Tsujimoto Y.; Homeda Y., Higuchi M., Tsujimoto Y.; Complete amino acid sequence and mutliform transcripts encoded by single copy of mouse NotCh2 gene."; Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lardelli M., Lendahl U.;
"Motch A and Motch B-two mouse Notch homologues coexpressed in a wide variety of tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.; "Murine notch homologs (N1-4) undergo presenilin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Martin D.I.;
"Inhibition of granulocytic differentiation by mNotchl.";
Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [5]
DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brain Res. Mol. Brain Res. 29:263-272(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 316-1518 FROM N.A.
STRAIN-C57BL/6 X CBA; TISSUE-Embryo;
MEDLINE-93178563; PubMed-8440332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99396706; PubMed-10393120;
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MEDLINE-97075110; PubMed-8917536;
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                CVPGYSGDOC 753
                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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SEQUENCE FROM N.A.
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apoptotic programs (By similarity). May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation.

SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and

SUBCELLULAR LOCATION: Type I membrane protein. Following

proteolytical processing NICD is translocated to the nucleus.
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in the brain, liver, kidney, neuroepithelia, somites, optic vesicles and branchial arches, but

-1. DEVELOPMENTAL STAGE: Expressed in the embryonic ventricular zone, the postnatal ependymal cells, and the choroid plexus throughout end postnatal development.

-1. PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand bliding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane.

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PTM: Phosphorylated.

-i- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
-i- SIMILARITY: CONTAINS 34.5 BGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 2 LIN/NOTCH REPEATS.
-i- SIMILARITY: CONTAINS 6 ANK REPEATS.

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EMBL; D32210; BAA22094.1; -. EMBL; X68279; CAA48340.1; -. EMBL; U31881; AAC52924.1; -. MGD; MGI:97364; Notch2 P16109; 1FSB. HSSP;

InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx.hydroxyl.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR000142; EGF-2.
InterPro; IPR001881; EGF_Ca. InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR000800; Notch.
Pfam; PF00008; EGF; 35.
Pfam; PF00023; ank; 6. Pfam; PF00066; notch; 2. PRINTS; PR00010; EGFBLOOD. PRINTS; PR01452; NOTCH.

SMART; SM00248; ANK; 4.
SMART; SM00179; EGF_CA; 22.
SMART; SM00001; EGF_like; 12.
SMART; SM00004; NL; 3.

PROSITE; PS50088. ANK_REPEAT; 4.
PROSITE; PS50029; ANK_REP_REGION; 1.
PROSITE; PS000022 SCF_1; 33.
PROSITE; PS01186; EGF_2; 27.
PROSITE; PS01187; EGF_CA; 22.
PROSITE; PS01187; EGF_CA; 22.
TRECEPTOR; Transcription regulation; Activator; Differentiation; Developmental protein; Repeat; ANK repeat; EGF-like domain; Transmembrane; Glycoprotein; Signal; Phosphorylation;

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POST-TRANSLATIONAL PROCESSING.

RA MEDLINE-97386453; PubMed-9244302;

RA Blaumuchler C.M., Ol H., Zagouras P., Artavanis-Tsakonas S.;

RI Tracellular cleavage of Notch leads to a heterodimeric receptor on the plasma membrane.";

RL Cell 90:281-291(1997).

RL Cell 90:281-291(1997).

RN EDENINE-99180765; PubMed-10079256;

A Banks A., Lethan R.S., Mitsladis E., Henrique D., Carcanglu M.-L.,

RN BANKS A., Lethan B.S., Mitsladis E., Henrique D., Carcanglu M.-L.,

RN HEDLINE-99180765; PubMed-10079256;

A Banks A., Lethan B.S., Mitsladis E., Henrique D., Carcanglu M.-L.,

RN HEDLINE-99180765; PubMed-10079256;

A Banks A., Lethan I. Sand D., 1sh-Horowitz D., Artavanis-Tsakonas S.;

RN HEDLINE-99180765; PubMed-10079256;

A Banks A., Lethan Ingands of the Notch released notch intracellular open 1 jagaedl and Deltal to regulate cell-fate determination.

Companion (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus.

Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity).

Companion (NICD) it forms a transcriptional activation and apoptotic programs (By similarity).

Companion (NICD) it forms a transcriptional activator complex with apoptotic programs (By similarity).

Companion (NICD) it forms a transcriptional activator complex with a proceeding and later.

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Companion (NICD) it forms a probably linked by disulfide bronds (By similarity).

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Companion (NICD) it forms a probably linked by disulfide by the probably 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stifani S., Blaumueller C.M., Redhead N.J., Hill R.E.,
Artavanis-Tsakonas S.;
"Human homologs of a Drosophila enhancer of split gene product define
a novel family of nuclear proteins.";
                                                                                                                                                                                                                                                                                                                                                                          Lemasson I., Devaux C., Mesnard J.M.; "Partial sequence of EGF-11ke repeat domain of human Notch2 mRNA."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (hN2).
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                         Correa R.G., Camargo A.A., Moreira E.S., Simpson A.J.; "Human Notch2, a novel member of cell-fate determining NOTCH
                                                                                                                                                                                                     "Complete human notch 2 (hN2) cDNA sequence.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
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  204721; Q9H240; Q99734;
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                                                                                      Homo sapiens (Human)
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2).
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@license.
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CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 4.

EGF-LIKE 6.

EGF-LIKE 6.

EGF-LIKE 7.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 9.

EGF-LIKE 9.

EGF-LIKE 10.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 12.

EGF-LIKE 13.

EGF-LIKE 14.

EGF-LIKE 14.

EGF-LIKE 17.

EGF-LIKE 17.

EGF-LIKE 18.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 13.

EGF-LIKE 14.

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN NOTCH EXTRACELLULAR TRUNCATION (BY SIMILARITY)
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RX MEDILINE-21331789; PubMed=11438922;
RA ITVID D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;
Rx Expression patterns of Notch1, Notch2, and Notch3 suggest multiple development.";
Texpression patterns of Notch1, Notch2, and Notch3 suggest multiple development.";
To Comp. Neurol. 436.167-181(2001)
To J. Comp. Neurol. 436.167-181(2001)
To J. Comp. Neurol. 436.167-181(2001)
To J. Gomp. Neurol. 436.167-181(2001)
To G. J. Sapped. 436.167-181(2001)
To J. Gomp. Neurol. 436.167-181(2001)
To J. Gomp. Asperse and 440 Junearly 100-1816
To J. Gomp. Asperse And 440 Junearly 100-1816
To J. Subult. 440-187. It is more highly localized to heart, liver and kidney.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                         Weinmaster G., Roberts V.J., Lemke G.; "Notch2: a second mammalian Notch gene.";
                                                                                                                                                                            MEDLINE-93202015; PubMed=1295745;
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EGF-like.
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EGF_Ca.
EGF_II.
Laminin_EGF.
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InterPro; IPR001438;
InterPro; IPR002049;
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                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY.
                                                                                                                    SEQUENCE FROM N.A.
                                                                 NCBI_TaxID=10116;
                                                                                                                                                   TISSUE-Brain;
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BGF-LIKE 3.

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InterPro; IPR000800; Notch.

Pfam; PF00008; BGF; 35.

Pfam; PF00006; notch; 2.

Pfam; PF00006; notch; 2.

R Pfam; PF00006; notch; 2.

R PRNWTS; PR00010; EGFELOOD.

R PRINTS; PR00011; EGFELAMININ.

R SMART; SM0019; EGF_CA; 22.

SMART; SM00001; EGF_Like; 10.

SMART; SM00001; EGF_Like; 10.

R SMART; SM00001; EGF_Like; 10.

R SMART; SM00001; EGF_Like; 10.

R PROSITE; PS00010; ASX_HYDROXIL; 4.

R PROSITE; PS00010; ASX_HYDROXIL; 22.

R PROSITE; PS01186; EGF_2; 26.

R PROSITE; PS01187; EGF_CA; 22.

R PROSITE; PS01187; EGF_CA; 22.

R PROSITE; PS01187; EGF_CA; 22.

M Receptor; Transcription regulation; Activator; Differentiation; M Developmental protein; Repeat; ANK repeat; EGF_like domain; Iransmembrane; Glycoproent; NW repeat; EGF_like domain; ISTANSMEMBER 1 SCHIN 26. 2471 NPTENDENT FORTER MARTHER MART
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LIN/NOTCH 2.
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ANK 2.
ANK 3.
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                                                                                                                                                                                                              hyaluronic acid.
SUBCELLULAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS: At least 4 isoforms; V0 (shown here), V1, V2 and V3; are produced by alternative splicing.
TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 are expressed in the central nervous system, and in a number of mesenchymal and epithelial tissues; the major isoform v2 is restricted to the
                                                                                                                                                                             FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds.
                                                                                             SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
                                                                                                                                                                                                                                                                                                            AND 342-348.
TISSUE-Spinal cord,
MEDLINE-92062692; PubMed-1720020;
Perides G., Biviano F., Bignami A.;
Interaction of a brain extracellular matrix protein with hyaluronic
                                            Limmermann D.R.; ^{\prime} "Versican V2 is a major extracellular matrix component of the mature
                                                                                                                                                                                                                                                                                        central nervous system.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
  SEQUENCE FROM N.A. (ISOFORMS VO; V1; V2 AND V3)
                                                                                                                                                            acid.";
Biochim. Biophys. Acta 1075:248-258(1991)
                                                                bovine brain.";
J. Biol. Chem. 273:15758-15764(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF060457; AAC24359.1; --
EMBL; AF060458; AAC24360.1; --
EMBL; AF060459; AAC24360.1; --
EMBL; AF060459; AAC2436.1; --
HSSP; POL113.2; 1EPG.
InterPro; IPR000152; ASX_hydroxyl.
InterPro; IPR0001561; EGF-11ke.
InterPro; IPR001891; EGF-2.
InterPro; IPR001891; EGF-Ca.
InterPro; IPR001806; Ig_HKC.
InterPro; IPR003006; Ig_HKC.
InterPro; IPR003006; Ig_like.
InterPro; IPR003006; Ig_like.
InterPro; IPR003008; Ig_like.
InterPro; IPR00308; Inik.
            TISSUE-Forebrain;
MEDLINE-98288320; PubMed-9624174;
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Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
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IG_like; 1.
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SM00410;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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PGCV_BOVIN STANDARD;
P81282; 077609; 077610; 077612;
P81282; 077609; (Rel. 37, ceated)
16-0CT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
16-OCT-2011 (Rel. 40, Last protecursor (Large fibroblast protecoglycan)
Chondroitin sulfate protecoglycan core protein 2) (PG-M) (Glial
hyaluronate-binding protein) (GHAP).
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  Query Match 86.0%;
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DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS00015; C_TYPE_LECTIN_1; 1.

DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

DR PROSITE; PS01180; EGF_2; 1.

DR PROSITE; PS01180; EGF_2; 1.

DR PROSITE; PS01181; EGF_2; 1.

DR PROSITE; PS01181; EGF_2; 1.

WW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; WW Slygnal; Repeat; EGF_11ke domain; Calcium; Immunoglobulin domain; "T SIGNAL 1. 20 POTENTIAR.

T CHAIN 21 320 POTENTIAR.
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EGF-LIKE 2, CALCIUM-BINDING.
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MEDLINE-93122792; PubMed-1478664;
IOZZO R.V., Naso M.F., Cannizzaro L.A., Wasmuth J.J.,
McPherson J.D.;
"Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chromosome 5 (5q12-5q14).";
Genomics 14:845-851(1992).
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MEDLINE-99181355; PubMed=7876137;
MEDLINE-99181355; PubMed=7876137;
MEDLINE-99181355; PubMed=7876137;
MEDLINE-99181355; PubMed=7876137;
MEXPRESSION of PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and human J. Biol. Chem. 270:3914-3918(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Placents;
MEDLINE-90059882; PubMed-2583089;
Zimmermann D.R., Rucslahti E.;
EMBO J. 8:2975-2981(1989).
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                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Butaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM V0).
MEDLINE-95105188; PubMed-7528942;
NASO M.F., Zimmernann D.R., IOSZO R.V.;
"Characterization of the complete genomic structure of the human yersican gene and functional analysis of its promoter.";
J. Biol. Chem. 269:32999-33008(1994).
                                                                                                                                                                                      PGCV_HUMAN STANDARD; PRT; 3396 AA.
P1361; P20754; Q9UNW5; Q13010; Q13189; Q15123;
01-JAN-1990 (Rel. 13, created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-GCT-2001 (Rel. 40, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein sulfate proteoglycan core protein) (GHAP).
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TISSUB-Glial tumor;

MEDLINE-95105187; PubMed-7806529;

Dours-Zimmermann M.T., Zimmermann D.R.;

"A novel 91/yosaminoflycan attachment domain identified in two alternative splice variants of human versican.";

J. Biol. Chem. 269:32998(1994).
                     Score 43; DB 1; Length 3381;
Pred. No. 19;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Lung fibroblast;
MEDLINE-88007514; PubMed=2820964;
Krusius T., Gehlsen K.R., Ruoslahtt E.;
A fibroblast chondroitin sulfate proteoglycan clectin-like and growth factor-like sequences.";
J. Blol. Chem. 262:13120-13125(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM V1).
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Query Match
Best Local Similarity 70.00,
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PROSITE; PS01187; EGE_CA; 1.
PROSITE; PS00613: LINK; 2.
PROSITE; PS00615: C_TYPE_LECTIN_1; 1.
Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; S1gnal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid; Alternative splicing.
SIGNAL.
Pfam; PF00047; ig; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
PRINTS; PR000109; Xlink; 2.
PRINTS; PR000109; EGFBLOOD.
PRODOM; P0000918; Link; 2.
SMART; SM00032; CCP; 1.
SMART; SM00019; EGF_CR; 1.
SMART; SM00109; EGF_CR; 1.
SMART; SM00019; EGF_Like; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
PROSITE; PS00010; ASX_HYDROXIL; 1.
PROSITE; PS01010; ASX_HYDROXIL; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
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                                                                                                                                                                                                                                 TISSUE SPECIFICITY OF ISOFORMS.

MEDLINE-96213482; PubMed-8627343;

MEDLINE-96213482; PubMed-8627343;

MEDLINE-96213482; PubMed-8627343;

Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;

J. Dours-Ession of versican isoforms in brain tumors.";

J. Neuropathol. Exp. Neurol. 55:528-533(1996).

-!- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the requiation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: At least 5 isoforms; V0 (shown here), V1, ALTERNATIVE PRODUCTS: At least 5 isoforms; V0 (shown here), V1, V2, V3 and Vint; are produced by alternative splicing.

TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expressed in normal brain, gliomas, medulloblastomas, schwannomas, neurofibromas, and menningiomas; V2 is restricted to normal brain and gliomas; v3 is found in all these tissues except
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 medulloblascoms.
--- DEVELOPMENTAL STAGE: Disappears after the cartilage development.
--- SIMILARITY: CONTAINS 1 INMUDOMALIN-LIKE V-TYPE DOMAIN.
--- SIMILARITY: CONTAINS 2 LINK DOMAINS.
--- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
--- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
--- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
--- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
--- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                             Lemire J.M., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.,
                                                                         "Versican/PG-M isoforms in vascular smooth muscle cells.";
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
                                                                                                                                                          Perides G., Lane W.S., Andrews D., Dahl D., Bignami A.; "Isolation and partial characterization of a glial hyaluronate-binding protein."; J. Biol. Chem. 264:5981-5987(1989).
    OF 3333-3396 FROM N.A. (ISOFORM VINT)
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IPR000436; Sushi_SCR_CCP
                  TISSUE-Aortic smooth muscle;
MEDLINE-99327053; PubMed-10397680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000152; Asx_hydroxyl InterPro; IPR000561; EGF-like.
                                                                                                                                    TISSUE-Brain;
MEDLINE-89174663; PubMed-2466833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003006; Ig_MHC.
InterPro; IPR001304; Lectin_C.
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EMBL; X1598; CAA34128.1; --
EMBL; S52488; AAB24878.1; --
EMBL; U2655; AA67565.1; --
EMBL; U2655; AA67661.1; --
EMBL; U26845; AAA68437.1; --
PIR; S06014; S06014.
PIR; A29348; A29348.
PIR; A30538; A30538.
HSSP; P01122; 1ECF.
Genew; HGNC:2464; CSPG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
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                                                                                                                      PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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EGF-LIKE 1. EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL). C-TYPE LECTIN.

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PROSITE; PS01187; EGF_CA; 18.
Blottin; Alternative splicing; EGF-like domain; Repeat; Signal; Glycoprotein; Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-LIKE 2, CALCIUM-BINDING (PO EGF-LIKE 3, CALCIUM-BINDING (PO EGF-LIKE 4, CALCIUM-BINDING (PO EGF-LIKE 5, CALCIUM-BINDING (PO EGF-LIKE 6, CALCIUM-BINDING (PO EGF-LIKE 7, CALCIUM-BINDING (PO EGF-LIKE 9, CALCIUM-BINDING (PO EGF-LIKE 10, CALCIUM-BINDING (PO EGF-LIKE 11, CALCIUM-BINDING (PO EGF-LIKE 12, CALCIUM-BINDING (PO EGF-LIKE 13, CALCIUM-BINDING (PO EGF-LIKE 13, CALCIUM-BINDING (PO EGF-LIKE 13, CALCIUM-BINDING (PO EGF-LIKE 21, CALCIUM-BINDING (PO EGF-LIK
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         send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PROMOILO; EGFELGOD.
PRINTS; PROMOILS; EGFELAMININ.
SWART; SMOMOILS; EGF. A.
SWART; SMOMOILS; EGF. CA; 18.
SWART; SMOMOILS; EGF. CA; 18.
PROSITE; PROMOILO; EGF. 119.
PROSITE; PROMOILS; EGF. 1; 19.
                                                                                                                                                                                                                                                               nustric restrictions of the property of the pr
                                                          EMBL, L08692, AAA62164.1; --
EMBL, L08692, AAA62163.1; --
EMBL, X17530, CAA35571.1; --
EMBL, M17421; AA330050.1; --
EMBL, X17531; CAA35573.1; --
PIR, A29316; A29316.
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PROSITE; PS00577;
PROSITE; PS01180;
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dev. Biol. 146:89-99(1991).
-!- FUNCTION: FORM THE APICAL LAMINA, A COMPONENT OF THE EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: EXTRACELLULAR. IN VESICLES IN THE CYTOPLASM OF UNFERTILIZED EGGS, THEN TO THE BASE OF THE HYALIN LAYER THROUGHOUT DEVELOPMENT AND FINALLY IN THE APICAL LAMINA IN LATE
                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS: 2 ISOFORMS; IA (SHOWN HERE) AND IB; ARE PRODUCED BY ALTERNATIVE SPLICING. THE SMALL FORM (IB) LACKS 8 EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89196806; PubMed-2784773;
Hunt L.T., Barker W.C.;
"Avidin-like domain in an epidermal growth factor homolog from a sea
urchin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90112459; PubMed-2514273;
Delgadillo-Reynoso M.G., Rollo D.R., Hursh D.A., Raff R.A.;
"Structural analysis of the uEGF gene in the sea urchin stronglocentrotus purpuratus reveals more similarity to vertebrate than to invertebrate genes with EGF-like repeats.";
J. Mol. Evol. 29:314-327(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Fibropellins, products of an EGF repeat-containing gene, form a unique extracellular matrix structure that surrounds the sea urchin
                                                                                                                                                                                                                                                                                                       protein 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-87319677; PubMed-3498216;
Hursh D.A., Andrews M.E., Raff R.A.;
"A sea urchin gene encodes a polypeptide homologous to epidermal
growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND ZYGOTICALLY.
SIMILARITY: CONTAINS 21 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 CUB DOMAIN.
SIMILARITY: THE C-TERMINAL DOMAIN OF THIS PROTEIN IS SIMILAR
TO AVIDIN/STREPTAVIDIN.
                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibropellin I precursor (Epidermal growth factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 279-476 AND 781-1064 FROM N.A.
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MEDILINE-91285234; PubMed-2060714;
Bisgrove B.W., Andrews M.E., Raff R.A.;
"Fibropellins, products of an EGF repeat
                                                                                                                                                                                                          (Rel. 10, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 237:1487-1490(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FASEB J. 3:1760-1764(1989).
3115 CVPGYSGDQC 3124
                                                                                                                                                   STANDARD;
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NCBI_TaxID=7668;
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                                                                                                                                                                                                          01-MAR-1989
                                                                                                                 FBP1_STRPU
ID FBP1_STRPU
AC P10079;
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mouses.;

Mech. Dev. 112:157-160(2002).

1- FUNCTION: Receptor that may have an important role in cell/cell signaling during nervous system formation.

1- SUBCELLUIAR LOCATION: Integral membrane protein.

1- SUBCELLUIAR LOCATION: Integral membrane protein.

1- DEVELOPMENTAL STAGE: Predominantly expressed in the developing CNS, the emerging dorsal root ganglia and cranial ganglia. In the CNS, expression is uniform along the rostrocaudal axis. During gastrulation, it is expressed within the anterior neural ectoderm. At ElO, expression is strong in the ventricular zones (WZ) in all servors of the brain, and lower in the marginal zones (WZ) in all servors of the brain, and lower in the marginal zones (WZ) in all servors in VZ, lower in MZ, except in telecephalic MZ where it is strong in VZ, lower in MZ, except in telecephalic MZ where it is strong in VZ, lower in MZ, except in the cerebral hemispheres, and to a lesser extent in the tectum and cerebral hemispheres, and to a lesser extent in the fetal lungs, kidney and epithelia. In the newborn and postnatal stages, expression remains restricted to the VZ as well as in migrating and postnajatory cells throughout the brain.

1- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.

1- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAINS.

1- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.

2- SIMILARITY: CONTAINS 1 GAP DOMAIN.

2- SIMILARITY: CONTAINS 1 GAP DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                              Celsr3 is
                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-99418630; PubMed-10490098; MEDLINE-99418630; PubMed-10490098; MEDLINE-99418630; PubMed-10490098; Usui T., Shima Y., Shimada Y., Hirano S., Burgess R.W., Schwarz T.L., Takeichi M., Uemura T.; "Flamingo, a seven-pass transmembrane cadherin, regulates planar cell Planingo, a seven-pass transmembrane cadherin, regulates planar cell polarity under the control of frizzled."; cell 98:585-595(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed-11850187;
Tissir F., De-Backer O., Goffinet A.M., Lambert de Rouvroit C.A.;
"Developmental expression profiles of Celsr (Flamingo) genes in the
                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                 Formstone C.J., Barclay J., Rees M., Little P.F.R.; "Chromosomal localization of Celsr2 and Celsr3 in the mouse; Coandidate for the tippy (tip) lethal mutant on chromosome 9. Mamm. Genome 11:392-394(2000).
                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1913-2796 FROM N.A., AND TISSUE SPECIFICITY
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submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
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MGD; MGI:1858225; Celsr2.
InterPrc; IPR000152; Asx hydroxyl.
InterPrc; IPR002126; Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 2014-2920 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                 PubMed-10790539;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sapence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 2 precursor (Flamingo 1)
BY SIMILARITY.
BY SIM
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MISSING (IN ISOFORM IB).
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W. 2E569CA012ED6D09 CRC64;
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Pred. No. 9.1;
3; Mismatches 1
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Matches 6; Conservative
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CPLGFSGDNC 325
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1064 AA;
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P18844;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nerocrafte (Rel. 41, Last annotatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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BY SIM
                                      EGF-LIKE 8, CALCIUM-BINDING
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                                                                                                        SIMILARITY.
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SEQUENCE FROM N.A.
MEDLINE-89231705; PubMed-2714283;
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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1820 CVLGYYGDNC 1829
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NCBI_TaxID=8355;
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7B2_XENLA
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CADHERIN 1.
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LAMININ G-LIKE 2.
EGF-LIKE 5, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of a neuregulin-related gene, Don-1, that is highly expressed in restricted regions of the cerebellum and hippocampus."; Mol. Cell. Biol. 17:4007-4014(1997).
-i- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE RECEPTORS. CONCOMITANTLY RECRUITS BRBB1 AND ERBB2 CORECEPTORS, ERBULTING IN LIGAND-STIMILATED TYROSINE PHOSPHORYLATION AND ACTIVATION OF THE ERBB RECEPTORS. MAY ALSO PROMOTE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pro-neuregulin-2 precursor (Pro-NRG2) (Contains: Neuregulin-2 (NRG-2)
(Divergent of neuregulin 1) (DON-1)].
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                    -!- PTM: UNDERGOES PROTEOLYTIC MATURATION IN SECRETORY GRANULES AND THUS GENERATES POTENTIAL BIOACTIVE PEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Choroid plexus;
MEDLINE-97342638; PubMed-9199335;
Busfield S.J., Michnick D.A., Chickering T.W., Revett T.L., Ma J.,
Woolf E.A., Comrack C.A., Dussault B.J., Woolf J., Goodearl A.D.J.,
Gearing D.P.,
                                                   -i- FUNCTION: 7B2 IS A SECRETORY PROTEIN OF NEUROENDOCRINE CELLS.
REGULATION OF SECRETION IS, AMONG OTHER ENDOCRINE FUNCTIONS, A
POSSIBLE ROLE OF 7B2 AND ITS PUTATIVE PEPTIDES.
-i- SUBCELLULAR LOCATION: Neuroendocrine and endocrine secretory
Martens G.J.M., Bussemakers M.J.G., Ayoubi T.A.Y., Jenks B.G.; The novel pituitary polypeptide 7B2 is a highly-conserved protein coextressed with proopiomelanococrtin."; Eur. J. Biochem. 181.75-79(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97311398; PubMed-9168115;
Carraway K.L. III, Weber J.L., Unger M.J., Ledesma J., Yu N.,
Gassmann M., Lai C.;
"Neuregulin-2, a new ligand of ErbB3/ErbB4-receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS NRG2-5; NRG2-10 AND NRG2-16A).
STRAIN-C57BL/6; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 150-756 FROM N.A. (ISOFORMS DON-1M AND DON-1S).
                                                                                                                                                                                                                                                                                                                                                                     Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                          SEQUENCE 161 AA; 17992 MW; A6E32531A29D82FC CRC64;
                                                                                                                                                                                                                                                                                                      Neuropeptide; Cleavage on pair of basic residues. NoN-TER ^{\rm L}
                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        756 A.A.
                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                     EMBL; X15608; CAA33631.1; -.
                                                                                                                                                                                                                                                                                                                                                                     80.08;
                                                                                                                                                                                                                                                                                                                                                                                  50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 387:512-516(1997).
                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.0
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          1 CVIGXSGDXC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPVGKTGDGC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                    ; S03938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
NRG2_MOUSE
ID NRG2_MOUSE
AC P56974;
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PISSUE SPECIFICITY: HIGHEST EXPRESSION IN THE BRAIN, WITH LOWER LEVELS IN THE LUNG. IN THE CEREBELLUM, FOUND IN GRANULE AND DURKINJE CELLS.

DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTECLYIC PROCESSING. REGULATION OF THE PROTECLYIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN DIMERIZATION (BY SIMILARIY).

DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                    PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE STERRAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR FORM (BY SIMILARITY).

PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGYTGDRCQQFAMVNFSKHLGFELKEAEELYQKRVLTITGI
CVALLVVG -> NGFFGQRCLEKLPLRLYMPDPKQSVLMDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> NGFFGQRCLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGTGVSSSQWSTSPSTLDLN (IN ISOFORM DON-1S).
SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS A PROTECLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE FORM. THE MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY) ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; DON-1M, DON-1S/NRG2-5, NRG2-10 AND NRG2-16A (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
Growth factor; EGF-1ike domain; Immunoglobulin domain; Glycoprotein; Transmembrane; Multigene family; Alternative splicing.

1 19 BY SIMILARITY.
CHAIN 20 756 PRO-NEUREGULIN-2, MEMBRANE-BOUND FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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INTERNAL SIGNAL SEQUENCE (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
SER/THR-RICH.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
HSSP; Q12784; 1HRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 756;
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MISSING (IN ISOFORM NRG2-10)
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VGYTGDRCQQFAMVNFSKHLGFELKE
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Pred. No. 15;
4; Mismatches
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1099246; Nr92.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR003598; Ig_C2.
InterPro; IPR002154; Neuregulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           756 AA; 82213 MW;
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Pfam; PF02158; Neuregulin; 1.
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN (BY SIMILARITY)
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Pfam; PF00047; 19; 1.
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307
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SMART; SM00408; IGc2;
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Matches 5; Conserv
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VARSPLIC
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1 CVIGXSGDXC 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 974-1021.

MEDLINE-86081810; PubMed-3000782;

MEDLINE-86081810; PubMed-3000782;

Simpson R.J., Smith J.A., Moritz R.L., O'Hare M.J., Rudland P.S.,

Martison J.R., Lloyd C.J., Grego B., Burgess A.W., Nice E.C.;

"Rat epidermal growth factor: complete amino acid sequence. Homology
with the corresponding murine and human proteins; isolation of a form

Eur. J. Blochem. 153:629-637(1985).
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                       EGF_RAT STANDARD; PRT; 1133 AA.
P07522; Q63183;
01-APR-1988 (Rel. 07, Created)
01-FBE-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pro-epidermal growth factor precursor (EGF) [Contains: Epidermal
                                                                                                                                                                                                                                                                                  TISSUE-Kidney;
MEDLINE-92398779; PubMed-1524680;
Price P.M., Saggi S.J., Safirstein R.;
"Cloning and sequencing of the rat preproepidermal growth factor CDNA: comparison with mouse and human sequences.";
DNA Cell Biol. 11:481-487(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dorow D.S., Simpson R.J.;
"Cloning and sequence analysis of a cDNA for rat epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   figure P.M.:
Price P.M.:
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 994-1108 FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Kidney;
MEDLINE-89016634; PubMed=3262867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001336; EGF 1...
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001083; Idl_receptor_rep.
Pfam; PF00008; EGF; Pfam; PF00058; Idl_recept_b; 7.
PRINTS; PR00009; EGFTGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P01132, IEGF.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U04842; AAB60436.1; -.
EMBL; X12748; CAA31241.1; -.
PIR; A25425; EGRT.
                                                                                                                                                                                                Rattus norvegicus (Rat).
   280 CPVGYTGDRC 289
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Kidney;
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HSSP; P01132
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                                                                                                        CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1 (INCOMPLETE).
EGF-LIKE 2. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 9.
EGF-LIKE 9.
EGF-LIKE 9.
                                                                                                                                                            (POTENTIAL).
                                                      Growth factor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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                                                                           PRO-EPIDERMAL GROWTH FACTOR EPIDERMAL GROWTH FACTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                > S (IN REF. 4).
C224A302E9578031 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GECNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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KL -> W (IN REF. 4).
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SIMILARITY.
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SIMILARITY.
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SIMILARITY.
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Pred. No. 22;
3; Mismatches
                                                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                           SIMILARITY
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                                                                      POTENTIAL.
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SWART; SM00179; EGF_CA; 2.
SWART; SM00001; EGF_like; 6.
FROSITE; PS00010; ASX_HYDROXYL; 3.
FROSITE; PS01020; EGF_l; 1.
FROSITE; PS01180; EGF_l; 6.
FROSITE; PS01180; EGF_CA; 3.
EGF_like domain; Repeat; Growth fa
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CALCIUM-BINDING (POTENTIAL).

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CALCIUM-BINDING (POTENTIAL).

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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS50088: ANK_REP_REGION; 1.
PROSITE; PS50027; ANK_REP_REGION; 1.
PROSITE; PS00021: EGF_1; 34.
PROSITE; PS00122: EGF_1; 34.
PROSITE; PS01187: EGF_2; 28.
PROSITE; PS01187: EGF_CA; 22.
Developmental protein neurogenesis; Repeat, ANK repeat;
Developmental protein; Neurogenesis; Repeat, ANK repeat;
Developmental protein; Neurogenesis; Repeat, ANK repeat;
CHAIN 1 20 POTENTIAL.
SIGNAL 1 20 NEUROGENIC LOCUS NOTCH HOWOLOG PROTEIN 1.
CHAIN 21 1724 POTENTIAL.
TRANSMEM 1725 1747 POTENTIAL.
                                                                                                                                                                                                                                                     **REDULINE-Y41200VC1; FULDED-2017-31,

**A zebrafish homologue of the Drosophila neurogenic gene Notch and

**Is pattern of transcription during early embryogenesis.";

**Is pattern of transcription during early embryogenesis.";

**Mech. Dev. 43:87-100(1993).

**DEVELOPMENT MAY BE INVOLVED IN THE FORMATION OF THE EMBRYO DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF THE NEURLY PLATE, NOTOCHORD AND BRAIN VESICLES.

**IS STAGES.** During gastrulation is differentially expressed, accumulating predominantly in the prechordal mesoderm and notochord. At the end of gastrulation, expressed along the anterior-posterior axis including the developing neural plate and differentiating mesoderm. Also present in the developing brain and head regions.

**IS STMILMARITY: CONTAINS 3 LIN/NOTCH REPEATS.**

**IS IMILMARITY: CONTAINS 6 ENF. REPEATS.**

**IS IMILMARITY: CONTAINS 6 ANK REPEATS.**
                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID-7955;
              01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 1 precursor.
NOTCHIA OR NOTCH.
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INTERPRO; IPR000152; ASX_hydroxyl.
INTERPRO; IPR0000152; ASX_hydroxyl.
INTERPRO; IPR000015; EGF-1ike.
INTERPRO; IPR0001881; EGF_2.
INTERPRO; IPR001881; EGF_1I.
INTERPRO; IPR001881; EGF_II.
INTERPRO; IPR000800; Notch.
Pfam; PF00006; EGF; 36.
Pfam; PF00006; EGF; 36.
Pfam; PF00006; ONCH.
PRINTS; PR00019; EGFELCOD.
PRINTS; PR001452; NOTCH.
SMART; SM00179; EGFELCOD.
SMART; SM00019; EGFELCOD.
SMART; SM00001; EGFELCOD.
SMART; SM00001; EGFELCOD.
SMART; SM00001; EGFELCOD.
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HSSP; P00740; 1EDM.
ZFIN; ZDB-GENE-990415-173; notchla.
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MEDLINE=94128602; PubMed=8297791;
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REP STRAIN-BERKEADAN N.A.

RAY SEQUENCE FROM N.A.

RAY MEDIINE-20196006; PubMed-10731132;

RADIAN-20196006; PubMed-10731132;

RADIAN-20196006; PubMed-10731132;

RADIAN-2019606; PubMed-10731133;

RADIAN-2019606; PubMed-10731133;

RADIAN-2019606; PubMed-10731133;

RADIAN-2019606; PubMed-10731133;

RADIAN-2019606; PubMed-20731133;

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RADIAN-2019606; PubMed-20731133;

RADIAN-2019606; PubMed-2073113;

RADIAN-2019606; PubMed-2073113;

RADIAN-2019606; PubMed-2073113;

RADIAN-2019606; PubMed-2073113;

RADIAN-2019606; PubMed-2073113;

RADIAN-2019606; PubMed-20731;

RADIAN-2019606; PubMed-20731;

RADIAN-2019606; PubMed-2073;

RADIAN-2019606; PubMed-2
                                                                                                                                                   STRAIN-Oregon-R: TISSUE-Embryo;
MEDLLINE-88196890; Pubmed-3149249;
KOPCZYNSKI C.C., Alton A.K., Fechtel K., Kooh P.J., Muskavitch M.A.T.;
"Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes a protein related to blood coagulation factors and epidermal growth factor of vertebrates.";
Genes Dev. 2:1723-1735(1988).
                                                             Vaessin H., Bremer K.A., Knust E., Campos-Ortega J.A.;
"The neurogenic gene Delta of Drosophila melanogaster is expressed in
neurogenic territories and encodes a putative transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Embryo;
MEDLINE-87218537; PubMed-3107986;
Knust E., Dietrich U., Tepass U., Bremer K.A., Weigel D., Vaessin H.,
                                        SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "EGF homologous sequences encoded in the genome of Drosophila melanogaster, and their relation to neurogenic genes."; EMBO J. 6:761-766(1987).
     Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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                                                                                                    with EGF-like repeats.";
EMBO J. 6:3431-3440(1987).
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SEQUENCE FROM N.A.
            NCBI_TaxID=7227;
                                                   TISSUE-Embryo;
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Diptera; Brachycera;
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Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
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                                                                                             15 REQUEED FOR THE CORRECT SEPARATION OF NEGRAL AND BEIDERMALL
CELL LINEAGES.

1- SUBCELLULAR LOCATION: Type I membrane protein.

1- TISSUE SPECIFICITY: DEPECTED IN ALL AREAS WITH NEUROGENIC
ABILITIES, FOR EXAMPLE THE NEUROGENIC ECTODERM AND THE PRINORDIA
OF THE SENSE ORGANS. LATER EXPRESSION IS RESTRICTED TO THOSE CELLS
THAT HAVE ADOPTED A NEURAL FATE.

1- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY.
EXPRESSION IS HIGHEST EARLY IN EMBRYONIC DEVELOPMENT (STAGE 5) AND
REDUCES TO A LOW LEVEL DURING LARVAL STAGES.

1- TED INNER PART OF EMBRYO IS ONE OF THE FIRST STEEPS OF CNS
THE INNER PART OF EMBRYO IS ONE OF THE FIRST STEEPS OF CNS
DEVELOPMENT IN INSECTS, THIS PROCESS IS UNDER CONTROL OF THE
NEUROGENIC GENES.

1- MISCELLANGOUS: NOTCH AND SERRATE MAY INTERACT AT THE PROTEIN MAY
COMPETE FOR BINDING WITH THE NOTCH PROTEIN.

1- SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                    Drosophila melanogaster.";
Development 110:1905-914(1990).
-i- FUNCTION: ESSENTIAL FOR PROPER DIFFERENTIATION OF ECTODERM. DL
IS REQUIRED FOR THE CORRECT SEPARATION OF NEURAL AND EPIDERMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ke domain; Glycoprotein; Signal.

POTENTIAL:

NEUROGENIC LOCUS DELTA PROTEIN.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

OTOPINATAL.

STOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00022; EGF_1; 9.
PROSITE; PS01186; EGF_2; 9.
PROSITE; PS01187; EGF_CA: 0.
Developmental protein; Differentiation; Neurogenesis; Repeat; Transmembrane; EGF-11ke domain; Glycoprotein; Signal.
Haenlin M., Kramatschek B., Campos-Ortega J.A.;
The pattern of transcription of the neurogenic gene Delta of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
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EMBL; Y00222; CAA68369.1; --
EMBL; AE003725; AAF55657.1; --
EMBL; X05140; CAA28786.1; --
PIR; X0570; S00670.
PIR; A26637; A26637.
HSSP; P00740; 1EDM.
FlyBase; FBGD00000463; Dl.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000152; Asx_hydroxyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00011; EGFLAMININ.
SMART; SM00051; DSL; 1.
SMART; SM000179; EGF_CA; 4.
SMART; SM00001; EGF_LA; 5.
PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS00022; EGF_L; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_II.
InterPro; IPR002049; Laminin_EGF.
Pfam; PF00008; EGF; 1.
Pfam; PF01414; DSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000561; EGF-11ke.
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EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 8.
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
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A -> S (IN REF. 3).
G -> A (IN REF. 3).
G -> A (IN REF. 3).
S -> T (IN REF. 3).
T -> A (IN REF. 3).
T -> A (IN REF. 1).
C -> N (IN REF. 1).
G -> N (IN REF. 1).
G -> N (IN REF. 1).
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N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
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V -> L (IN REF. 1)
A -> R (IN REF. 1)
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BY SIMILARITY
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Pred. No.
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Maximum Match 100%
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q8vd07 mus musculu Q9vc97 drosophila O35452 mus musculu O54796 mus musculu Q21756 caenorhabdi Q8vtp0 halocynthia O16004 lytechinus Q8t5z1 caenorhabdi Q8t5z2 caenorhabdi Q8t5z2 caenorhabdi Q8t5z2 caenorhabdi Q8t5z3 caenorhabdi Q9tpn0 caenorhabdi Q9tpn0 caenorhabdi Q9tpn0 caenorhabdi Q9tpn0 caenorhabdi Q9tpn0 caenorhabdi Q9tpn0 caenorhabdi
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eg OB	111 111 111 111 55 55 57 113
% Query Match Length DB	1200 1200 4006 4114 372 1162 191 191 191 193 194 615 9615 9615
% Query Match I	1000.0 990.0 990.0 990.0 984.0 884.0 884.0 884.0 884.0 884.0 884.0 884.0
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ALIGNMENTS

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	PRT;	Created)	ast se	factor.		Cran	SCIU				, , , ,	EMBL/6		roxyı.	U		4 1 1	-tonda	r					(VI.: II)	NOWN	CNOWN	IKNOWN.	MW;	1	Pred 2; M	
1 100	Q8VD07 PRELIMINARY;	(TrEMBLrel. 20,	(TrEMBLrel. 20,	_	Mus musculus (Mouse).	Eukaryota; Metazoa; Chordata;	Mammalia; Eutheria; Rodentia;	NCBI_TaxID=10090;	SEQUENCE FROM N.A.	TISSUE=KIDNEY;	Strausberg R.;	Submitted (DEC-2001) to the	, AAH17	InterPro; IPR000152; Asx_nydroxy1	IPR000561;	IPR001336;	InterPro;					SMART; SM00181;	SMART; SMOOI/9; EGF_CA;	SMART; SP	PROSITE; PSUCOIO;	PROSITE; FS00222;	PROSITE: PS01187; EGF	SEQUENCE 1200 AA		Best Local Similarity 80.0%; Matches 8; Conservative	
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PRINTS; PR00010; EGFBLOOD
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RE Addas W. N.A.

RE Addas W. D. Celliker S.E., Holt F.M., Evans C.A., Gocayne J.D.,

RA Addas W.D., Celliker S.E., I. P. W., Hoskins R.A., Galle R.F.,

Rannatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Recorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Barter E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Cawley S., Dallec T., Barckstein P., Brottler P.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davlas P.C.,

Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Brosler C., Gabriellan A.E., Garp N.S., Galbart W.M., Glasser K.,

RA Bourbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Weal M.-H., Ibegwam C.,

Liu X., Mattei B.E., Kodire C.D., Kraft C., Keniston J.R.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., Morris J., Morshy D.M., Nelson D.R.,

RA Hoson D.R., Nelson K.A., Mayno M., Nusskern D.R., Paceler F., Shen H.,

RA Britaka S.M., Pittman G.S., Pan S., Pollard J., Puri V., Wang X.,

Rainer E., Speier R., Percia T., Order W., Stupes R.,

Reinert K., Remington K., Saunders R., Vencer E., Wang X.,

RA Hallsan S.M., Welson R.A., Weinstock G.M., Weinschold J.,

RA Hallsan S.M., Weinschoff T., Wein D., Shan R.,

RA Hallsan S.M., Weinschoff T., Wein D., Shan R.,

Reinert R., R
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"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterrygota; Neoptera: Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                     PRT; 2146 AA.
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                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
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InterPro; IPR000561; EGF-1ike.
InterPro; IPR000181; EGF_2.
InterPro; IPR00183; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001791; Laminin_GF.
Pfam; PF00008; EGF; 26.
Pfam; PF00008; EGF; 36.
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1 CVIGXSGDXC 10
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CRB OR CG6383.
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                                                                                      PROSITE; PS00010; ASX HYDROXYL; 16.
PROSITE; PS00010; ASX HYDROXYL; 16.
PROSITE; PS01186; EGF_1; 25.
PROSITE; PS01187; EGF_CA; 17.
Calcium-binding; EGF_1ike domain; Glycoprotein; Hydroxylation; Repeat. SEQUENCE 2146 AA; 233570 MW; 8E23B9E32B761115 CRC64;
                                                                                                                                                                                                                                                                                                                        Gaps
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Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,

Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.,

"Sequence of the mouse major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                     Length 2146;
                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF_1; UNKNOWN_19.
PROSITE; PS01186; EGF_2; 19.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
EGF-1ike danair; Glycoprotein.
SEQUENCE 4006 AA; 435471 MW; 553FBE873498A4FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region.";
Submitted (CCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF030001; AAB82015.1; -.
HSPP; PO2671; IFZD.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR00181; Fibrinogen_C.
InterPro; IPR003961; FN_III.
Pfam; PF00008; EGF: 15.
Pfam; PF000147; fibrinogen_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                Score 45; DB 5;
Pred. No. 15;
3; Mismatches
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PRINTS; PRO0011; EGFLAMININ. SMART; SM00179; EGF_CA; 11. SMART; SM00001; EGF_Ike; 16. SMART; SM00282; LamG; 3.
                                                                                                                                                                                                                                                                  90.08;
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SMART; SM00101; EGF_11ke; 2.
SMART; SM00186; FBG; 1.
SMART; SM00060; FN3; 24.
                                                                                                                                                                                                                                                                  Query Match 90.0
Best Local Similarity 60.0
Matches 6; Conservative
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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569 CAVGYSGDRC 578
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532 CAVGYSGDDC 541
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Sawada H., Sakai N., Abe Y., Tanaka E., Takahashi Y., Fujino J., Kodama E., Takizawa S., Yokosawa H.; "A Novel Sperm Receptor VC70, Consisting of 12 EGF-like Repeats, Is Degraded by the Ubiquitin-Proteasome Pathway during Ascidian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO61740; BAB72021.1; -
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000142; EGF_11.
InterPro; IPR00101439; EGF_11.
InterPro; IPR00101439; EGF_11.
R PRINTS; PR00010; EGFBLCOD.
R SWART; SW00181; EGF; 14.
R SWART; SW00241; ZP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   86.0%; Score 43; DB 5; Length 372; 60.0%; Pred. No. 5.9;
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PROSITE; PS0123: EGF_1; UNKNOWN_13.
PROSITE; PS01186; EGF_2; UNKNOWN_10.
SEQUENCE 1162 AA; 124499 MW; 26F57DE32B1A8E6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                           "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: U58746; AAB00626.1;
HSSP; P01132: 1A3P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
Murray J., Le T.T.;
"The sequence of C. elegans cosmid R05G6.";
Submitted (MAX-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                 InterPro: InterPro: EGF-like.
InterPro: IPR000561; EGF-like.
SMART; SM00181; EGF; 7.
PROSITE; PS00022; EGF_l; UNKNOWN_7.
PROSITE; PS01186; EGF_2; 6.
EGF-like domain; Glycoprotein; Hypothetical protein.
EGF-like domain; Glycoprotein; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
vitelline coat component HrVC120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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60.0%; Pred. No. 19;
iive 3; Mismatches
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596 CLFGFSGDHC 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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66 CFLGWSGDSC 75
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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Q8WTP0;
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STRAIN-FI BETWEEN C57BL6, AND CBA;

X MEDLINE-94216385; PubMed=7512972;

A Matsumoto K., Saga Y., Ikemura T., Sakakura T., Chiquet-Ehrismann R.;

A matsumoto K., Saga Y., Ikemura T., Sakakura T., Chiquet-Ehrismann R.;

The Distribution of tenascin-X is distinct and often reciprocal to "The Distribution of tenascin-X is distinct and often reciprocal to "The Distribution of tenascin-X is distinct and often reciprocal to "The Distribution of tenascin-X is distinct and often reciprocal to "The Distribution of tenascin-X is distinct and often reciprocal to "In that of tenascin-X" is BA24436.1; -..

REMBL, AB01026; BAA24436.1; -..

REMBL, AB01026; BAA24436.1; -..

RIGHEPRO; IPR001561; EGF-11ke.

RIGHEPRO; IPR001561; FIDINOGEN—C.

RIGHEPRO; IPR001561; FIDINOGEN—C.

REMBL, PF001041; fibrinogen—C; 1.

REMBL, PF001041; fibrinogen—C; 1.
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NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-F1 BETWEEN C57BL6, AND CBA;
STRAIN-F1 BETWEEN C57BL6, AND CBA;
MEDLINE-99014231; PubMed-9795100;
Ikuta T., Sogawa N., Ariga H., Ikemura T., Matsumoto K.;
"Structural analysis of mouse tenascin-X: evolutionary aspects of reduplication of FNIII repeats in the tenascin gene family.";
Gene 217:1-13(1998).
                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; ___ience 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SMO0060; FN3; 24.

PROSITE; PS00022; EGF_1; UNKNOWN_19.

PROSITE; PS01166; EGF_2; 17.

PROSITE; PS00514; FIBRIAG_C_DOMAIN; 1.

EGF-1ike domain; Glycoprofealn.

SEQUENCE 4114 AA; 447268 MW; 45FE7AD5145881A1 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
Hypothetical 39.1 kDa protein.
R0566.9.
Caenorhabditis elegans.
                          01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00181; EGF; 7.
SMART; SM00001; EGF_11ke; 2.
SMART; SM00186; FBG; 1.
SMART; SM00060; FN3; 24.
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532 CAVGYSGDDC 541
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                                                                                                                                                                               NCBI_TaxID=10090;
                                                                            Tenascin-X.
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Q21756;
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Gaps

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09 RAPPO
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Matches

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PRT;
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EMBL; AF491463; AAM09703.1; -.
NON_TER 1 1
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60.08;
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60.0%;
                                                                                                  Genetics 0:0-0(2002).
EMBL; AF491462; AAM09702.1;
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Best Local Similarity 60.0°,
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Caenorhabditis briggsae.
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Caenorhabditis briggsae.
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53 CPLGYSGDYC 62
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[1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Best Local Similarity
Matches 6; Conserv
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                                STRAIN-PB800;
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NON_TER
SEQUENCE
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Q8T5Z2
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                                                                                                                                                   Lytechinus Variegatus (Sea urchin).
Eukaryota: Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
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08T521;
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ENVATYORAL METAZOA: Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
NCBL_TAXID=6238;
                                                                                                                                                                                                                                                                                                         "Identification and localization of a sea urchin Notch homologue: insights into vegetal plate regionalization and Notch receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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PROSITE; PS01186; EGF_2; 25.
PROSITE; PS01187; EGF_CA; 20.
ANK repeat; Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 2531 AA; 273982 MW; 5BF42BEC627CA303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 5; Length 2531;
Pred. No. 42;
3; Mismatches 1; Indels
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                                                                                01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO1452; NOTCH.

SMART; SM00248; ANK; 5.

SMART; SM00179; EGF_CA; 23.

SMART; SM00001; EGF_Like; 11.

PROSITE; PS50089; ANK_REPERT; 10.

PROSITE; PS50089; ANK_REP_REGION; 2.

PROSITE; PS00010; ASX_HYDROXYL; 21.
                                                                                                                                                                                                                                                                                                                                                       Development 124:3363-3374(1997).
EMBL; AF000634; AAB82088.1; -.
HSSP; POII32; IEGF.
InterPro; IPR002110; ANK.
InterPro; IPR00152; ASX hydroxyl.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                       MEDLINE-97454256; PubMed-9310331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR000800; Notch.
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60.0%;
                                                                                                                                                                                                                                                                                           Sherwood D.R., McClay D.R., "Identification and localiz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00066; notch; 3.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR00010; EGFBLOOD
PRINTS; PR01452; NOTCH.
                                                   PRELIMINARY;
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615 CPVGTSGDNC 624
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                                                                                                                                                                                                                       NCBI_TaxID=7654;
                                                                                                                                     Notch homolog
                                                                                                                                                                                                                                                                                                                                             regulation.
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                                                016004
                                                                       016004
              RESULT 7
016004
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Graustein A., Gaspar J.M., Walters J.R., Palopoli M.F., "Levels of DNA polymorphism vary with mating system in the nematode genus Caenorhabditis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Graustein A., Gaspar J.M., Walters J.R., Palopoli M.F.;
Levels of DNA polymorphism vary with mating system in the nematode
genus Caenorhabditis..;
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Rhabditidae; Peloderinae; Caenorhabditis.
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"Levels of DNA polymorphism vary with mating system in the nematode
genus Caenorhabditis.";
Genetics 0:0-0(2002).
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                                                                                                                                                         191
20977 MW; ZEEB21B5FFA46470 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 AA; 20943 MW; ZEEB21B5F47FB470 CRC64;
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Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pred. No. 4.7;
                                                                                                                                                                                                                                                                                        3; Mismatches
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SEQUENCE FROM N.A.
MEDLINE-98165391; PubMed-9425132;
Haddon C., Smithers L., Schneider-Maunoury S., Coche T., Henrique D.,
                 Gaps
                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                      'Multiple delta genes and lateral inhibition in zebrafish primary
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15;
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                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO0010; ASX_HYDROXYL; UNKNOWN_2.
PROSITE; PSO1022; EGF_1; UNKNOWN_9.
PROSITE; PSO1186; EGF_2; 7.
PROSITE; PSO1186; EGF_2; 7.
Calcium-binding; EGF-1ike domain; Glycoprotein; Repeat.
SEQUENCE 615 AA; 67592 MW; CA18004428F5603C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Notch-like transmembrane receptor (Fragment)
GLP-1.
                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                 1;
                                                                                                                                            615 AA.
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                3; Mismatches
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Pred. No. 1
  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZEIN; ZDB-GENE-980526-114; dlb.
InterPro; IPR00152; Asx_hydroxyl.
InterPro; IPR01774; DSL.
InterPro; IPR000561; EGF-like.
InterPro; IPR000142; EGF_2.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001438; EGF_II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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EMBL; AF006488; AAC41241.1; -.
HSSP; P00740; 1EDM.
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50.0%;
60.08;
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SMART; SMOUD11; DSL; 1.
SMART; SMOO179; EGF_CA; 3.
SMART; SMOOOD1; EGF_LIKe; 5.
 Best Local Similarity 60.0
Matches 6; Conservative
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nes 5; Conservative
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194 CLVGWOGDYC 203
                                          1 CVIGXSGDXC 10
                                                           | :|:||:|
56 CPLGYSGDYC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 7.
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                                                                                                                                                                                                                                                                                    Cyprinidae; Danio.
NCBI_TaxID-7955;
                                                                                                                                                                                                                DeltaB.
DLB OR DELTAB.
                                                                                                                                                                                                                                                                                                                                                                                                      neurogenesis.
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                                                                                                                RESULT 13
057409
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Q9GPM9
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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-HK104, AND HK105;
Graustein A., Gaspar J.M., Walters J.R., Palopoli M.F.;
"Levels of DNA polymorphism vary with mating system in the nematode genus Caenorhabditis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Graustein A., Gaspar J.M., Walters J.R., Palopoli M.F.;
"Levels of DNA polymorphism vary with mating system in the nematode genus Caenorhabditis.";
Genetics 0:0-0(2002).
EMBL; AF491458; AAM09698.1; -.
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                                                                    84.0%; Score 42; DB 5; Length 193; 60.0%; Pred. No. 4.7; 1; Indels iive 3; Mismatches 1; Indels
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                                         42135BBBE8BE02C5 CRC64;
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194 AA; 21275 MW; 07313C8ABD9C65C5 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                             193 AÀ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                             PRT;
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EMBL; AF491459; AAM09699.1; -.
EMBL; AF491461; AAM09701.1; -.
                            193
21178 MW;
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 EMBL; AF491460; AAM09700.1;
                                                                  Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                Caenorhabditis briggsae.
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Caenorhabditis briggsae.
                                                                                                                            1 CVIGXSGDXC 10
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56 CPLGYSGDYC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CVIGXSGDXC 10
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55 CPLGYSGDYC 64
                            193 1
193 AA;
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                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6238;
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                            NON_TER
SEQUENCE
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SEQUENCE
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Best Local S
Matches 6
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SEQUENCE
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                NON_TER
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Q8T5Z3
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Search completed: July 2, 2003, 07:28:39 Job time: 42.3333 secs
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430 CPLGYSGDYC 439
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              Ob
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                                            RAY MEDLINE=2110341; PubMed=11156985;

RA Rudel D., Kimble J.;

"Conservation of glp-1 regulation and function in nematodes.";

"Conservation of glp-1 regulation and function in nematodes.";

R. Genetics 157:639-654(2001).

DR RESP: Poll32; lag6.

RIGEPRO; IPRO00152; Ax_hydroxyl.

RIGEPRO; IPRO00152; Ax_hydroxyl.

RIGEPRO; IPRO000152; Ax_hydroxyl.

RIGEPRO; IPRO00042; EGF-11ke.

B. InterPro; IPRO00042; EGF-11ke.

RIGEPRO; IPRO00049; EGF-11ke.

RIGEPRO; IPRO00040; EGF-11ke.

REAM: PRO0004; EGF: 4.

PRINTS; PRO0001; EGF-14.

RINTS; PRO0001; EGF-14.

RART; SM00001; EGF-14.

SMART; SM00001; EGF-11ke; 4.

SMART; SM00001; EGF-11ke; 4.

SMART; SM00001; EGF-11ke; 4.

RESPIRE: PS500010; AX, HYDROXYL; UNKNOWN-1.

RESPIRE: PS500010; AX, HYDROXYL; UNKNOWN-1.

REPROSITE; PS001010; AX, HYDROXYL; Transmembrane.

NO SPONTEME DESPIREDENT; Repeat; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Matazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Reladerinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 963 AA; 106394 MW; 52BF80010E12FB57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Notch-like transmembrane receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1270 AA
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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR000742; EGF-2.
InterPro; IPR001881; EGF-Ca.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR000800; Notch.
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Best Local Similarity 60.00,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CVIGXSGDXC 10
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   NCBI_TaxID=6238;
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Q9GPN0
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS5008 "ANK REPEAT; 3.
PROSITE: PS50297; ANK REP_REGION; 1.
PROSITE: PS00010; ASX_HIVDNOXYL; 2.
PROSITE: PS001186; EGF_2; UNKNOWN_10.
PROSITE: PS01187; EGF_2; 8.
PROSITE: PS01187; EGF_CA; 1.
ANK REPEAT; Re
Pfam; PF00008; EGF; 10.
Pfam; PF00066; notch; 3.
PRINTS; PR000011; EGFLAMININ.
PRINTS; PR01452; NOTCH.
SWART; SM00248; ANK; 5.
SWART; SM00181; EGF: 12.
SWART; SM00101; EGF. 110.
SWART; SM00001; EGF. 110.
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Best Local Similarity 60.00,
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